

SEQUENCE LISTING

<110> Zyskind, Judith
Ohlsen, Kari L.
Trawick, John
Forsyth, R. Allyn
Froelich, Jamie M.
Carr, Grant J.
Yamamoto, Robert T.
Xu, H. Howard

<120> GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
ESCHERICHIA COLI

<130> ELITRA.001DV1

<150> 09/492,709

<151> 2000-01-27

<150> 60/117,405

<151> 1999-01-27

<160> 485

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 159

<212> DNA

<213> E. Coli

<400> 1

caggtggtat ggaaacccaa aatggagacg ggaagctgaa ccagatagtt actggaggtg	60
atcaccagca gatgaaataa cgataaccag aacaacgcct tatagcgttg agtttgcgag	120
aaaacgttca tattgtacct ttttgattaa ccattgggg	159

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<211> 696

<212> DNA

<213> E. Coli

<220>

<221> misc_feature

<222> (1)...(696)

<223> n = A,T,C or G

<400> 2

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gtcaactact caaacgtgga accgagcgat ttcgttcaga ccttctcacg ccgtaatggt	180
ggggaagcga ccagcggatt ctttgaagt cggaaaaacg aaaccaaaga aaatggaatt	240
cgtctttccg agcgtaaaga gacactgggt gatgtgacgc accgcattct gacagtgccg	300
attgocgagg atcaggtggg gatgtattac cagcagccag ggcaacaact ggcaacctgg	360

attgttcttc	cgggacaata	cttcatgatg	ggcgacaacc	gcgacaacag	cgcggaacagc	420
cgttactggg	gctttgtgcc	ngaagcgaat	ctgggtcggtc	nggcaacggc	tatctggatg	480
aacttcgata	accaagaagg	cgaatggccg	aatgggtctgc	cctaantcgc	attggcgntt	540
ccnttaatan	ccacttcctt	cncctttgtcc	ccttatggca	acacttaatt	tattntaaan	600
taatcncccg	tggctnacaa	atccccgcct	tttnttaaaa	atttcccna	anttaaggtt	660
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<211> 681

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<400> 3

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acgtaagcgg	atggagtggc	cggaacctc	atagtgaccg	cccaccagtt	ggcctgcatc	180
gctttgtagc	gtacgcgcgg	catttgcaat	aagattcaga	tactcagact	cttccggggc	240
cttcgccagc	ataaaagagg	aggatgctcg	cgtatgcagc	aactgctcca	gcgcaaattg	300
cagccgcggt	tgagtatcac	tgaataaagg	atcgttttcg	tcaatcaaat	gtggctgagc	360
aaatatttcc	tgatagctat	cggtatcagg	aaccagggtca	cgccatgcaa	gtttcgtaat	420
ggtcaaagtt	gatgtttttt	agtctgttgt	caaagccgcn	attataccng	taaccggcac	480
tacagcacac	gtagaaagca	cccgacaata	ctcctggcat	gggcgttaaa	gctcacagga	540
tggagatctt	ttcttcactg	gcctaaaaag	ctgatattct	gtaaagagtt	acacngtaac	600
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gaaagtatct	ggttaagaag	c				681

<210> 4

<211> 289

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<213> E. Coli

<400> 4

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tacttaacgg	agaaccatta	agccttagga	cgcttcacgc	catacttga	acgagcctgc	180
ttacggtctt	taacgccgga	gcagtcaagc	gcaccacgta	cggtgtggta	acgaacaccc	240
gggaggtctt	taacacgacc	gtcacggatc	aggatcacgg	agtgtctct		289

<210> 5

<211> 815

<212> DNA

<213> E. Coli

<220>

<221> misc_feature

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<223> n = A,T,C or G

<400> 5

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aaatatgaag	ggggagagcc	cttatagacc	aggtagtaca	cgtttggtta	gggggcctgc	120
atatggcccc	ctttttcact	tttatactct	tgccggtttta	tgccgggcag	atcacatctc	180

cgaggatttt	agaatggctg	aaattaccgc	atccctggta	aaagagctgc	gtgagcgtag	240
tggcgaggc	atgatggatt	gcaaaaaagc	actgactgaa	gctaacggcg	acatcgagct	300
ggcaatcgaa	aacatgcgta	agtccggtgc	tattaaagca	gcgaaaaaag	caggcaacgt	360
tgctgctgac	ggcgtgatca	aaacccaaat	cgacggcaac	tacggcatca	ttctggaagt	420
taactgccag	actgacttcg	ttgcaaaaga	cgctggtttc	caggcggttcg	cagacaaagt	480
tctggacgca	gctgttgctg	gcaaaatcac	tgacgttgaa	gttctgaaag	cacagttcga	540
agaagaacgt	gttgcgctgg	tagcgaaaat	tggtgaaaac	atcaacattc	gccgcgttgc	600
tgcgctggaa	ggcgacgttc	tgggttctta	tcagcacggg	gcgcgtatcg	gccgttctgg	660
ttgctgctaa	aagcgctgac	gaagaactgg	ttaaaccacat	cgttttgacc	tttgttgcaa	720
gccaagccag	aattcagaga	aactttccgc	ttcaccggag	gtcccacca	cangganccc	780
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<210> 6
 <211> 403
 <212> DNA
 <213> E. Coli

<400> 6

caacactatt	ttgttgaccg	gaaaatggaa	cactttccgc	aatgcctggt	gctatcacgc	60
ttaaaccatt	tcattgcgat	ttacacagaa	cggacgtcct	gtcgcagtat	attaagtcgt	120
cgatagaaac	aagcattgaa	aggcacagca	gtagtcaaac	agtgtgaaac	gctactggcg	180
ccttacagcg	caaaaaggct	ggtgactaaa	aagtcaccag	ccatcagcct	gatttctcag	240
gctgcaaccg	gaagggttgg	cttattttaac	ttcaacttca	gcgccagctt	cttcagagc	300
ttttttcagt	gcttctgctg	cgtctttgct	cacgccttct	ttcagagcag	ccggtgcaga	360
ttctaccagg	tcttttagctt	ctttcagacc	caggccagtt	gcg		403

<210> 7
 <211> 149
 <212> DNA
 <213> E. Coli

<400> 7

gagctttttt	cagtgtctct	gcgtcgtctt	tgctcacgcc	ttctttcaga	gcagccggtg	60
cagattctac	caggtcttta	gcttctttca	gaccagggcc	agttgcgcc	cgtagctgtt	120
tgataacagc	aactttgtta	gcgccagca				149

<210> 8
 <211> 742
 <212> DNA
 <213> E. Coli

<220>

<221> misc_feature
 <222> (1)...(742)
 <223> n = A,T,C or G

<400> 8

ccatctgtcc	attgagcggg	cagtttgtgc	aacactat	ttgtgaccgg	aaaatggaac	60
actttccgca	atgcctgttg	ctatcacgct	taaaccattt	cattgcgatt	tacacagaac	120
ggacgtcctg	tcgcagtata	ttaagtcgtc	gatagaaaca	agcattgaaa	ggcacagcag	180
tagtcaaaca	gtgtgaaacg	ctactggcgc	cttacagcgc	aaaaaggctg	gtgactaaaa	240
agtcaccagc	catcagcctg	atttctcagg	ctgcaaccgg	aagggttggc	ttattttaact	300
tcaacttcag	cgccagcttc	ttccagagct	tttttcagtg	cttctgcgtc	gtctttgtct	360
acgccttctt	tcagagcagc	cggtgcagat	tctaccaggt	ctttagcttc	tttcagaccc	420
aggccagttg	cgccacgtac	tgctttgata	acagcaactt	tgtagcgcc	agcagctttc	480
agaattacgt	cgaattcagt	tntttcttca	gcagcttcaa	ccgggccagc	agctacagct	540
acagcagcag	caagcggaaa	caccgaattt	ttcttccatt	gcagagatca	gttctacaac	600

cgtccattac	agacatagct	gcaactgctt	caatgatttt	gatcttttagt	ggatagacat	660
ttaaattggt	cctgaattat	caagaaataa	gtnttatacg	taagccgaaa	tgcgttaaaa	720
aagataactg	ngattaaagc	ag				742

<210> 9
 <211> 421
 <212> DNA
 <213> E. Coli

<400> 9						
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aaagtcacca	gccatcagcc	tgattttctca	ggctgcaacc	ggaagggttg	gcttatttaa	120
cttcaacttc	agcgccagct	tcttccagag	cttttttcag	tgcttctgcg	tcgtctttgc	180
tcacgccttc	tttcagagca	gccggtgcag	attctaccag	gtcttttagct	tctttcagac	240
ccaggccagt	tgcgccacgt	actgctttga	taacagcaac	tttgtttagcg	ccagcagctt	300
tcagaattac	gtcgaattca	gttttttctt	cagcagcttc	aaccggggcca	gcagctacag	360
ctacagcagc	agcagcgga	acaccgaatt	tttcttccat	tgcagagatc	agttctacaa	420
c						421

<210> 10
 <211> 126
 <212> DNA
 <213> E. Coli

<400> 10						
agagcttttt	tcagtgtctc	tgcgctgtct	ttgctcaagc	cttcttttcag	agcagccggt	60
gcagattcta	ccaggtcttt	agcttctttc	agaccagggc	cagttgcgcc	acgtactgct	120
ttgata						126

<210> 11
 <211> 262
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(262)
 <223> n = A,T,C or G

<400> 11						
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tctaccaggt	cttttagcttc	tttcagaccc	aggccagttg	cgccacgtac	tgctttgata	180
acagcaactt	tgttagcgcc	agcagctttc	agaattacgt	cgaattcagt	tttttcttca	240
gcagcttcaa	ccgggccagc	ag				262

<210> 12
 <211> 202
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(202)
 <223> n = A,T,C or G

<400> 12

gcgcataccc	tgcagcatcg	gcccgatgga	gatcaggctg	gcagaacgct	gtaccgcttt	60
gtaggtggtg	ttaccggtgn	tcagatccgg	gaagatgaac	acggtagcgc	gacctgcaac	120
cggagagttc	ggcgctttgg	attncgcaac	gtcagccatt	accgcagcgt	cgtactgcag	180
cggaccggcg	atcatcaggt	ca				202

<210> 13
 <211> 261
 <212> DNA
 <213> E. Coli

<400> 13						
tctaggagta	agaatagctt	caaattcagc	agttgacagt	ggcataaacg	taactgggtga	60
cttttgcccg	gcatgacgcc	gggctttttt	tattattccg	tgacttccag	cgtagtgaag	120
gcaaacttct	cgccatcaaa	tagccctga	ctggttagtt	ttagcgcggg	gatcactggc	180
agagaaaagaa	acgccatctg	aataaacggc	tcacgaggta	acggaccgca	ttcacggggcg	240
gcggctttca	aggcgtcaat	t				261

<210> 14
 <211> 224
 <212> DNA
 <213> E. Coli

<400> 14						
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tttttattat	tatggggaag	gtgttattta	tgagtttcat	ttatgccgta	acgacaatga	120
actcggaat	tagtataagc	agcgcgagaa	taataatcat	tgtgcaaag	ctaatttaat	180
taatactatt	taaatattat	tttgagcata	tgacataag	gttg		224

<210> 15
 <211> 232
 <212> DNA
 <213> E. Coli

<400> 15						
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tgctgatttt	tattattatg	gggaagggtg	tatttatgag	tttcattttat	gccgtaacga	120
caatgaactc	gggaattagt	ataagcagcg	cgagaataat	aatcattgtg	caaagtctaa	180
tttaattaat	actattttaa	tattattttg	agcatatgca	cataagggtg	gg	232

<210> 16
 <211> 212
 <212> DNA
 <213> E. Coli

<400> 16						
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cctcgggtac	ttatgctgat	ttttattatt	atggggaagg	tgttatttat	gagtttcatt	120
tatgccgtaa	cgacaatgaa	ctcgggaatt	agtataagca	gcgcgagaa	aataatcatt	180
gtgcaaatgc	taatttaatt	aatactattt	aa			212

<210> 17
 <211> 433
 <212> DNA
 <213> E. Coli

<400> 17						
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caggccataa	atgccaccag	aattatcgtc	aaccaaccaa	ttgctgaaac	gccaaagcagc	120
agcggggcgg	agagctgttt	cagttcggcg	ggtaaccctt	caatccattt	gccgccagtc	180
cacagcaaca	tgatgcctct	gtacaaccct	aacgtgccaa	gggtggcaac	aatggcaggg	240
atctttagcc	acgcgaccag	gacaccgttg	aaaaatcccg	cgagcaaacc	aagcagtaaa	300
gtcgcgacac	aagcaacagg	tagtgaatat	cctgcgttca	gtaacatccc	caacagcacc	360
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gtcgcgcca	ttg					433

<210> 18
 <211> 658
 <212> DNA
 <213> E. Coli

<400> 18

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tccttccccg	ttgaggacac	cggttgtca	ggttgaccat	acgtttaagt	gacaaccccg	120
ctgcaacgcc	ctctgttatc	aattttctgg	tgacgtttgg	cggtatcagt	tttactccgt	180
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ggacgcgata	atgaaaacgt	tattaccaa	cgtaataacg	tctgaagggt	gttttgaaat	420
tggtgtcact	atcagtaacc	cagtattttac	tgaagatgcc	attaacaaga	gaaaacaaga	480
acgggagcta	ttaaataaaa	tatgcattgt	ttcaatgctg	gctcgtttac	gtctgatgcc	540
aaaaggatgt	gcacaatgaa	ttcagcattt	gtgcttggtc	tgacagtttt	tcttgtttcc	600
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<210> 19
 <211> 588
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(588)
 <223> n = A,T,C or G

<400> 19

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attgttaact	ggttaacgtc	acctggaggc	accaggcact	gcatcacaaa	attcattgtt	180
gaggacgcga	taatgaaaac	gttattacca	aacgttaata	cgtctgaagg	ttgttttgaa	240
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cgggagagcc	agttgatatt	gcagtcagtg	ttcacaggac	aatgcangag	tgtatgactg	480
cagcaaccgg	aacagaaaat	tcccggtaac	tgttaccggg	tcgataaagt	tattcaccag	540
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<210> 20
 <211> 101
 <212> DNA
 <213> E. Coli

<400> 20

gatccagcaa	gaagatgcgg	ttgtaccgtc	atcacgcaga	tgcgcaaagc	tactcagcaa	60
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<210> 21
 <211> 465
 <212> DNA
 <213> E. Coli

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<400> 21
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cgagggtgcag ttcgcccata cccgcgatga tgggtctggtt agattcttcg tcagtccata    180
cacggaaaga cgggtcttct ttagccagac ggcccagagc cagaccattt ttttcctggt    240
cagctttggt tttcggttca actgcgatgg agattaccgg ctcagggaat tccatacgtt    300
ccagaatgat cggcgcaccc gggtcacaca ggggtgtcacc agtggttacg tctttcagac    360
cgatagcagc agcgatgtcg cccgcgogaa cttctttgat ctcttcacgt ttgttagcgt    420
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<210> 22
 <211> 859
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(859)
 <223> n = A,T,C or G

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gaatacccat gtctactacc gggtagcctg ccagcggacc tgctttcagc tgttcctgga    180
tacctttatc aacggccggg atgtattcgc cagggattac accaccttta atgtcgttga    240
tgaactcgta gcctttcggg tttgaaccgg gctccagcgg gtacatgtcg ataacaacat    300
gaccatactg accacgacca ccagactggt tgcgctgttt accttcaaca tcggttaactt    360
tctggcggat agtttcacgg taagcaacct gcggtttacc tacgttcgct tcaacggtga    420
attcacgctt catacgggtca acgatgatgt cgagggtgcag ttcgcccata cccgcgatga    480
tgggtctggtt agattcttcg tcagtccata cacggaaaga cgggtcttct ttagccagac    540
gggccaanagc cagaccattt ttttcctggt cagctttggt tttcggtcaa ctgcgatgga    600
gattacgggc tcanggaatt tccatacctt ccaggaatga tcggcgcatt ccggtcaaac    660
angngtacc aggggggttac ntntttttaa nancgattgc cagcancgga tntnnccgn    720
gccnaacttc tttggaacnn tttaccggtt ggtaaccngc cttttnaacn atccaaccga    780
aaaagngtta anngccantt ttccngngt tnanntncgg nttccngaa ntaaccncc    840
cggggtnaac ccngnaaaa                    859
  
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<210> 23
 <211> 269
 <212> DNA
 <213> E. Coli

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<400> 23
ctttcttaaa gccttcttta aaggcgatag aagcagccag tttaaacgcc agttcagagg    60
agtcaacgtc atggtaagaa ccgaagtgc gacgaatacc catgtctact accgggtagc    120
ctgccagcgg acctgcttct agctgttctt ggataccttt atcaacggcc gggatgtatt    180
cgccagggat tacaccacct ttaatgtcgt tgatgaactc gtagcctttc gggtttgaac    240
cgggctccag cgggtacatg tcgataaca                    269
  
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<210> 24
 <211> 330
 <212> DNA

<213> E. Coli

<400> 24

gttttgggga	gatgtaagg	ctaactgaa	tggctgcatt	ccttggttaa	ggaaaaacga	60
atgactgatt	gccgatacct	gattaaacgg	gtcatcaaaa	tcattcattgc	tgttttacag	120
ctgacccctc	tggtcttata	acacaaggaa	acgtacttaa	ggcgccgtcc	gtgaaccagt	180
cggacgcacc	tttaataact	ataaataagt	gtctgggcag	atactatata	aattaactta	240
gtgaatgatt	atgctaattg	catcaattaa	ataaatataa	tggcggttaag	gcttcccagt	300
aataataatta	atactctact	tccagagtag				330

<210> 25

<211> 471

<212> DNA

<213> E. Coli

<220>

<221> misc_feature

<222> (1)...(471)

<223> n = A,T,C or G

<400> 25

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ctgacccctc	tggtcttata	acacaaggaa	acgtacttaa	ggcgccgtcc	gtgaaccagt	180
toggacgcac	ctttaataac	tataaataag	tgtctgggca	gatactatat	aaattaactt	240
agtgaatgat	tatgctaatt	tcattcaatta	aataaatata	atggcggtta	ggcttcccag	300
taataataatt	aatactctac	ttccagagta	gaatattaaa	ttttatccgc	gtggtgcac	360
agcacaatt	tatccacaaa	ctgttcttct	gtctcgacat	gcccccgat	ctttnacaaa	420
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<210> 26

<211> 379

<212> DNA

<213> E. Coli

<220>

<221> misc_feature

<222> (1)...(379)

<223> n = A,T,C or G

<400> 26

natctgantg	gctgcattcc	ttgtttaagg	aaaccogaat	gactgattgc	cgatacctga	60
ttaaaccgggt	catcaaaatc	atcattgctg	ttttacagct	gacccctctg	ttcttataac	120
acaaggaaac	gtacttaagg	tgcgtccggg	gaaccagtcg	gacgcacott	taataactat	180
aaataagtgt	ctgggcagat	actatataaa	ttaacttagt	gaatgattat	gctaattgtca	240
tcaattaaat	aaatataatg	gcgttaaggc	ttcccagtaa	tataattaat	actctacttc	300
cagagtagaa	tattaaattt	tatccgcgtg	gtgcatcagc	acaaatttat	cccacaactg	360
ttcttctgtc	tcgacatgc					379

<210> 27

<211> 799

<212> DNA

<213> E. Coli

<400> 27

aaagatgatg	tgatgagaaa	gtcaatttga	ataagacaat	attaagagct	aaaaaaatgt	60
caaaaaacac	taaatcaaaa	aataatggca	ttagaaaaata	taatgcgaaa	acggaggtga	120

aattagttta	tttcaaatga	ggaaaatctc	cgggcgaaaa	aaccgggaga	tgaaagtgtg	180
atgggtatca	aataaacaac	agaggagaaa	tttttaacgc	agccattcag	gcaaatacggt	240
taatcccatt	gcctggcgga	taagttgcgg	cttaacgcca	ggaagcgtgt	cggccagttt	300
caaaccaata	tcacgcagca	gttttttcgc	cggattggta	ccgaaaaaca	gatcgcggaa	360
tccctgcata	ccagccagca	tcaacgcgc	actgtgcttg	cggctacgct	catagcgacg	420
cagataaatg	tactgcccga	tgtctgggat	ccgtcgacct	gcagccaagc	ttgggctttt	480
cagcctgata	cagattaaat	cagaacgcag	aagcgggtctg	ataaaacaga	atttgccttg	540
cggcagtagc	gcggtggtcc	cacctgacct	catgccgaac	tcagaagtga	aacgcccgtg	600
gcgcccgatg	gtagtgtggg	gtctcccat	gcgagagtag	ggaactgcc	ggcatcaa	660
aaaacgaaa	gctcagtcga	aagactgggc	ctttcgggtt	atctgggtgt	tgtcggtgaa	720
cgtctctga	gtaggacaaa	tccgcggga	gcggattttg	aacgttgcca	aacaaccggc	780
ccggaagg	gtgggggct					799

<210> 28
 <211> 636
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(636)
 <223> n = A,T,C or G

<400> 28						
aggggggtttg	ttgtgggcaa	tgatgcattt	aagttatcgt	ctgcagatag	aggagatatt	60
acaataaaca	acgaatcagg	gcatttgata	gtcaataaccg	caattctatc	aggagatata	120
gtcaactctaa	gaggaggaga	aattaggttg	gtattatagc	ttgtgcgcgc	catgattggc	180
gcgcaatttta	aacttagtgc	tttacatcgc	tattgtcttg	atttctttga	attattttat	240
aaattaaaaa	aacgactggt	atgtataagc	aaaggtcgaa	cgaaaaatac	attccaaata	300
aatgcttgct	taaatctcta	tatccttccc	cgaaaaatga	cacataaaat	tgagatattc	360
caaaaagaga	tactacaaat	aaagatgcct	ttattttatt	atttctaata	aaaatagaag	420
caataaaaaa	taataacaat	gatataaatc	taatgttttt	aaatatattg	tcttttatgt	480
tagtaatagt	cgttagtagt	tttgattctc	catatattac	gtgtagtttt	ttatatacat	540
ggaaataatt	ntctttatac	tgagacatca	caccatcatc	aatggaagt	ttgaagatgg	600
tgcttggttt	gctaaccaat	aaaagagtg	cattcg			636

<210> 29
 <211> 757
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(757)
 <223> n = A,T,C or G

<400> 29						
cagcggctgt	atttttagca	tggtttttta	ttggcggcta	tgctgccccg	ggagcataaa	60
gatgaaaaaa	acaacgatta	ttatgatggg	tgtggcgatt	attgtcgtag	tcggcactga	120
gctgggatgg	tggtaacgtc	acctctaaaa	aatagcaaa	gctgcctgtg	tgacgccttt	180
gtgcaatttta	agcgttaact	tttaatcttc	ctgtagataa	atagcacgac	aatcgacca	240
ataacggcaa	ccacgaagct	gccaaaattg	aagccatcga	ctttaccaa	gccaaacagc	300
gtgctgatcc	atccgcccgc	tacggcaccg	actatcccc	gcaggatagt	cataaagaat	360
ccacctccat	ctttacctgg	catgatccac	ttcgccagaa	taccggcaat	aagocaaaa	420
ataatccatg	acagaatgcc	cattgtttcc	tcacttatct	gttttgcat	agcgggttag	480
tcgctgataa	aaagcatagc	acaacatcgc	gagggcaaga	tttgtgacga	gcacacgga	540
ggtttttttt	gcgatggcgc	agaaattgcg	ccatcaacga	tcagtgataa	ttaccaacca	600

caaacatcat	gttcgttttc	cgtgtcataa	gaaccgtacg	ggattcacca	gatcttttat	660
cacttcaagc	cggcacttct	ggcaccagca	aagtcacg	cgtctctggt	tcataatcga	720
ccggaacgc	cattgctggt	attggtgaac	gtcacgg			757

<210> 30
 <211> 392
 <212> DNA
 <213> E. Coli

<400> 30						
aattacagaa	aaaggaggca	atatcgggta	aaggcattag	cccagcgaat	acgtcgggct	60
acaaatatta	ttgtgctgca	ggtgttttag	cgggttggtg	atccacaggt	tctaactgga	120
agaccacatc	gacctgatca	tcaaactgaa	tagcggcctg	ctcgtaagtt	tcctgggcgg	180
acaccggcgc	ggcatcggct	ttcatcatcc	gcaccattgg	gctgggctga	tagttggaaa	240
catggtagcg	cacgctatat	accggcccca	gtttacgatg	aaagccgttc	gccagttcct	300
gcgcctgatg	aatcgcggtt	tcaatcgctg	ccttacgcgc	tttgtcttta	taggcatccg	360
gctgcgccac	gcccagcgac	acagaacgaa	tt			392

<210> 31
 <211> 351
 <212> DNA
 <213> E. Coli

<400> 31						
ctatccttga	tgaaaccgcg	agcaaagata	ggtgattacg	tcattggtttt	acagaaaatt	60
acagaaaaag	gaggcaatat	cgggttaaagg	cattagcccg	acgaatacgt	cgggctacaa	120
atattattgt	gctgcagggtg	tttttagcggg	ttgttgatcc	acaggttcta	actggaagac	180
cacatcgacc	tgatcatcaa	actgaatagc	ggcctgctcg	taagtttcct	gggcggacac	240
cggcgcgcca	tcggctttca	tcattccgcac	cattgggctg	ggctgatagt	tggaacatg	300
gtagcgcacg	ctatataaccg	gccccagttt	acgatgaaa	ccgttcgcca	g	351

<210> 32
 <211> 762
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(762)
 <223> n = A,T,C or G

<400> 32						
aattatgaaa	cactgtctgg	aatcgtctga	atgacgggca	catttgcgag	cacgcatcca	60
gtaataacac	aggaaactat	tttatctacg	cgttagcgat	agactgcttg	catggcgaaa	120
ggaggtaagc	cgacgatttc	agcgggacgc	tgaaacggga	aagcccctcc	cgaggaaggg	180
gccataaata	aggaaagggt	catgatgaag	ctactcatca	tcgtggtgct	cttagtcata	240
agcttccccg	cttactaaga	ctaccagggc	gggggaaacc	ccgctctacc	ctcactcctg	300
aaagtatgcc	ttcacgataa	gattgtcaat	ccgcaggctt	tgtagtctgc	gatoctgcca	360
gcaaatattc	tttgcgagtc	gttacgcaat	aatcacagag	gaaactatct	tattcacgcg	420
ttagcgatag	actgcattca	gggcgaaagg	aggtaagccg	atgatttcag	cgggacgctg	480
aaacgggaaa	gcctctcccc	gagaagaggg	cttttaataa	ggaaagggtt	atgatgaagc	540
acgtcatcat	actggtgata	ctcttagtga	ttagcttcca	ggcttactaa	gaacaccagg	600
gggaggggga	aacctcttcc	taacctctac	ttctgaaatt	gggtgctatg	acgctggcgt	660
tactgcttan	cgctaccagt	ttgtctgccc	tggcggttgt	aacgccagat	cggtaaccgt	720
ttggatatatt	taatgaaagc	cgacaaatca	atcancgtga	cg		762

<210> 33

<211> 293
 <212> DNA
 <213> E. Coli

<400> 33

gcacatttgc	gagcacgcat	ccagtaataa	cacaggaaac	tattttatct	acgcgttagc	60
gatagactgc	ttgcatggcg	aaaggaggta	agccgacgat	ttcagcggga	cgctgaaacg	120
ggaaagcccc	tcccgaggaa	ggggccataa	ataaggaaag	ggtcgatgatg	aagctactca	180
tcatcgtggt	gctcttagtc	ataagcttcc	ccgcttacta	agactaccag	ggcgggggaa	240
accccgctct	accctcactc	ctgaaagtat	gccttcacga	taagattgtc	aat	293

<210> 34
 <211> 633
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(633)
 <223> n = A,T,C or G

<400> 34

atttacactt	tttacgaaat	catgggatca	ctaacaaaat	atcgcttgct	agtttatattg	60
tatggcagga	aagatatgcg	actgatatta	cagatcccca	aagtggagag	tttatgacca	120
ttaaaaataa	gatgttgctg	ggtgcgcttt	tgctggttac	cagtgccgcc	tgggccgcac	180
cagccaccgc	gggttcgacc	aatacctcgg	gaatttctaa	gtatgagtta	agtagtttca	240
ttgctgactt	taagcatttc	aaaccagggg	acaccgtacc	agaaatgtac	cgtaccgatg	300
agtacaacat	taagcagtgg	cagttgcgta	acctgcccgc	gcctgatgcc	gggacgcact	360
ggacctatat	gggtggcgcg	tacgtgttga	tcagcgacac	cgacggtaaa	atcattaaag	420
cctacgacgg	tgagattttt	tatcatcgct	aaaaaaagcc	ccctcatcat	gagggggaaa	480
tgcagacacc	ttgntatttt	ttattattag	ccacttgctc	gtcttgcttg	gtattaagtc	540
gtattttcacg	ttgattaatg	cnggtggctc	cagtgcgcca	gattaacttt	gtttggatcg	600
aagacgtagt	aactggctgg	ttatcggaat	tgg			633

<210> 35
 <211> 569
 <212> DNA
 <213> E. Coli

<400> 35

tatggcagga	aagatatgcg	actgatatta	cagatcccca	aagtggagag	tttatgacca	60
ttaaaaataa	gatgttgctg	ggtgcgcttt	tgctggttac	cagtgccgcc	tgggccgcac	120
cagccaccgc	gggttcgacc	aatacctcgg	gaatttctaa	gtatgagtta	agtagtttca	180
ttgctgactt	taagcatttc	aaaccagggg	acaccgtacc	agaaatgtac	cgtaccgatg	240
agtacaacat	taagcagtgg	cagttgcgta	acctgcccgc	gcctgatgcc	gggacgcact	300
ggacctatat	gggtggcgcg	tacgtgttga	tcagcgacac	cgacggtaaa	atcattaaag	360
cctacgacgg	tgagattttt	tatcatcgct	aaaaaaagcc	ccctcatcat	gagggggaaa	420
tgcagacacc	ttgttatttt	ttattattag	ccacttgctc	gtcttgcttg	ttattagtcg	480
tattttcacgt	tgattaatgc	ggttgccctc	agtgcgccag	atttaacttt	gtttgtatcg	540
tagacgtagt	aactggctgg	tatcggaat				569

<210> 36
 <211> 338
 <212> DNA
 <213> E. Coli

<400> 36

cgtattcaca	tccttttgat	tggtgataac	atgcgaatcg	gtattatattt	tccggttgta	60
atcttcatta	cagcggtcgt	atcttttagca	tggtttttta	ttggcgggcta	tgctgccccg	120
ggagcataaa	gatgaaaaaa	acaacgatta	ttatgatggg	tgtggcgatt	attgtcgtac	180
tcggcactgc	ctgggatggg	ggtaacgtca	cctctaaaaa	atagcaaagg	ctgcctgtgt	240
gcagcctttg	tgcaatttaa	gcgttaactt	ttaatcttcc	tgtagataaa	tagcacgaca	300
atcgaccaa	taacggcaac	cacgaagctg	ccaaaatt			338

<210> 37
 <211> 375
 <212> DNA
 <213> E. Coli

<400> 37						
ctgaatatatt	aaaaaggaaa	acgacatgaa	accgaagcac	agaatcaaca	ttctccaatc	60
ataaaatatt	tccgtggagc	atctttattat	tgaatataga	ggtttaactc	cggtaaaaaa	120
caaagaagca	ttgaatgcag	ggaaaaataa	tatggccata	aaaaacatcg	aaagaaactc	180
ttttaattta	acatgtaaac	gcattggttaa	tcctcatatc	acgggtggag	tgtaagaac	240
atacataaat	ggagtcattg	tttccctttt	ccatttatca	agttcctgtt	gccgttttag	300
tccatctcta	attgcatatt	tttaatttttc	tgataaatgg	cattgagcat	cgatttcatt	360
taaaacaact	gtaca					375

<210> 38
 <211> 446
 <212> DNA
 <213> E. Coli

<400> 38						
ttacgatagc	tattagtaaa	aataataagag	ttagctgtat	tggtatgtct	gtggcgaaat	60
tgactacott	cgtttttttg	attaagaatg	atctttattat	cgtaagtaaa	attacatgaa	120
tatttaaaaa	ggaaaacgac	atgaaaccga	agcacagaat	caacattctc	caatcataaa	180
atattttcgt	ggagcatttt	attattgaat	atagagggtt	aactccggtg	aaaaacaaag	240
aagcattgaa	tgacgggaaa	aataatatgg	ccataaaaaa	catcgaaaga	aactctttta	300
atttaacatg	taaacgcatt	gttaattcctc	atatcacggg	tgagtggtta	agaacataca	360
taaatggagt	catgttttcc	cttttccatt	tatcaagttc	ctgttgccgt	tttagtccat	420
ctctaattgc	atattttaat	ttttct				446

<210> 39
 <211> 392
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(392)
 <223> n = A,T,C or G

<400> 39						
tcaccccggt	gccgattttc	aggcatcctg	atttaactta	gcacccgcaa	cttaactaca	60
ggaaaacaaa	gagataaatg	tctaattcctg	atgcaaatcg	agccgatttt	ttaatcttta	120
cggactttta	cccgcctggg	ttattaattg	cactgtatc	cgggcgttcg	cccgttttaa	180
tcacaatagg	ctgtgtagcc	tgggcctggt	tctctttcac	ccgcgccaga	gcggcagcaa	240
tcgcatcttt	atctttgggt	gcaggttgaa	cggctgcgct	cttatgtcgt	tcaaggcgag	300
ccgctttttc	gcgctccaga	cgagcctggc	gcgcttcgaa	acgcgctttg	gcttctgcgg	360
cncgcttttc	ttcctgacga	atagccgcaa	tt			392

<210> 40
 <211> 208

<212> DNA
<213> E. Coli

<400> 40

taataacgct	atctgcggat	aaagcagaat	agggtggttaa	ccccagacat	aaaccgagga	60
aaataatggt	attgtatttc	ataatctatt	gttccttagc	gacagattgc	tgtctgctgg	120
ttcagtaagg	taccaggaga	aacttcagga	agcttggtact	cgacaatata	gtttgagttt	180
ttatctttgc	cccatgaaac	ctgtaatt				208

<210> 41
<211> 342
<212> DNA
<213> E. Coli

<400> 41

catcctcaat	acogttaaat	gcaacccgaa	cccccgttgt	ccctttgctg	cattcactta	60
acgtaatctg	aaaagggagc	gctggacttg	tgctaccggt	cgttggaaat	tgtctggcac	120
tggttttttg	gagatctacg	gtaaaattaa	gcgaatccga	tgagactgtg	cagccataat	180
cgaggacgcg	cccgctaatt	ttaataacgc	tatctgcgga	taaagcagaa	taggtggtta	240
accccagaca	taaaccgagg	aaaataatgt	tattgtattt	cataatctat	tggtccttag	300
cgacagattg	ctgtctgctg	gttcagtaag	gtaccaggag	aa		342

<210> 42
<211> 841
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(841)
<223> n = A,T,C or G

<400> 42

agatttactg	ccaattttccg	gcagatcgga	aagggttaaa	ccatattgat	ccataagggt	60
acgaatcacg	gctataccgc	caggcatggc	ttgagccatg	gcattaaatt	ccgcaaattc	120
gggogctgat	tcttcccacg	cggttatttt	ggcacacacc	agatccagca	aggggtnttc	180
aggatcgttg	agcagcagat	gatctaccag	ttncagcgcc	tgggtgtatt	gntccttggt	240
ctgaataccc	gnnagaaaag	gtgccacagc	anttagcttn	tctcctgctt	gcaagatgtc	300
tggaatngc	aatcattttt	tgcacttant	acgatgnaca	nongtaaaga	aatcgnattt	360
ttntatgccg	tcataacttt	acgtatgtan	cactttttgc	nattcnaaaa	aagaccattn	420
gctncaacac	gtaaatttna	ttgnccccna	catttanaac	ataaatgntt	aaaattttcc	480
ccccnccnna	ttttaagntn	ttnanagaat	ngggaattac	ctgcttttna	atgnactcan	540
anttttttng	naataattcc	tntatcnaaa	ctnnntttcn	cccaanagnc	nnccaaattn	600
cggtttnttn	nttnncnngg	cnttttttta	cccnanaann	tttattcaan	nocttttttg	660
tagnctattt	naagngnct	ttnttnnatt	aactttccnn	ttggncaaat	tttggcnnat	720
ttttatatan	aattntctta	tntcntaatt	tnggnanccc	cngatgnaan	tttatggngg	780
gantcccnnt	ccctntttta	tnnatgntct	gggntatttt	taaanccctn	attaannnan	840
c						841

<210> 43
<211> 215
<212> DNA
<213> E. Coli

<400> 43

aataactttt	cgtaggcag	ttttgggtgt	gagttgcaag	aggggagact	actgaataac	60
tcaagtttta	taatcgaggg	gaaaatgggt	atggcggttca	tagcaaaacg	coctcaacca	120

taaagggtcga	gggcgcttaa	gatgttaaaa	acccgctatc	cggttaaaaaa	caatgttcaa	180
ctaagggtcag	tgacattgcg	ctaaaaaagc	gaatt			215

<210> 44
 <211> 395
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(395)
 <223> n = A,T,C or G

<400> 44						
gcattattca	tgagaaatgt	gtatcgtaaa	tcaactgaaa	ttaacgcaac	catttgttat	60
ttaagggttta	attatctgtg	tgtgatattt	tattgaatgt	tttaaataatt	gtttttattg	120
gcattgctat	aatattggtt	atcattttgct	gaatggattc	agtcttaatg	agtgggtttt	180
taaggggacag	gcataagagta	atgatacgta	tgcataacca	acatctttac	tcattatgtc	240
attgaatgtt	gaccctatgt	gtttatgaag	gagaggtatt	ttcagttgat	ctggattgnt	300
aaattcatat	aatgcgctt	tgctcatgaa	tggatgccag	tatgtagtgg	gaaattataa	360
atattgaaat	agtcacaacta	cttctttatt	accaa			395

<210> 45
 <211> 883
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(883)
 <223> n = A,T,C or G

<400> 45						
ataatcaggt	aagaaaaggt	gcgcggagat	taccgtgtgt	tgcgatatat	tttttagttt	60
cgcggtggcaa	tacatcagtg	gcaataaaac	gacatatcca	gaaaaatata	cactaagtga	120
atgatattctt	ccgatttatc	ttaatcgitt	atggataacg	gcaaagggct	tcgttttttc	180
ctatactttat	tcagcactca	caaataaagg	aacgccaatg	aaaattatac	tctgggctgt	240
attgattatt	ttcctgattg	ggctactggt	ggtgactggc	gtatttaaga	tgatatttta	300
aaattaatta	atgtcatcag	gtccgaaaat	aacgagaata	tttcagtctc	tcacccctgtt	360
gcgctcctgt	catgtgcatt	gcttcatata	atcactggcg	caaggagcgc	cgcaggcgna	420
gnntgcncgn	cgncccacct	naccccatgc	cgaacttcag	aantgaaaac	nccntaacnc	480
cgatngtcgg	cggnggcctc	cccatgcnan	agtangggaa	ntgccangcg	nennattaaa	540
cgaaaggctn	attncaaaga	ctgggccttn	cntttatctg	atgtttgtcg	gagaacgctc	600
tcctgagnan	gacaaatncc	gccgggagcg	gatttgaacn	ttgcgaagca	accgnccna	660
aggngnngt	cntgacnccc	nctctanct	nnngccttc	ttttgcttna	angncctcct	720
ancngatggc	ctttttngcc	ntctacaaa	cnntttggtt	aatgcttnta	aaancctttc	780
cannntncaa	tcngtnntn	cccatccnnn	tnntgaaagn	ntnccnccn	tgtncantnt	840
anntnngggg	gnngngngcc	ggcggncccc	cccccccccc	ccc		883

<210> 46
 <211> 1024
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(1024)

<223> n = A,T,C or G

<400> 46

gtttatggat	aacggcaaag	ggcttcgttt	tttctatac	ttattcagca	ctcacaaata	60
aaggaacgcc	aatgaaaatt	atactctggg	ctgtattgat	tattttcctg	attgggctac	120
tggtagtgac	tggcgtat	aagatgatat	tttaaaatta	attaatgtca	tcagggtccga	180
aaataacgag	aataatttcag	tctctcatcc	tgttgcgctc	ctgtcatgtg	cattgcttca	240
tataatcact	ggcgcaagga	gogcgagag	tntccnant	nnnnntnntt	ntntnnctnn	300
nccttcacna	tncnnccn	nantnnatag	nncaccnntn	ttntcnnnn	gnccnctcc	360
nnncnnnnnn	ncatnnnatc	ccactnnntt	tntccannn	nnncnnnnntn	canncnacaa	420
antncnaccn	anntnacctt	atacnannc	nancnnnnnn	nnccactctn	netcgnnctc	480
cccnttcnac	nnccannnnn	cancnntcnn	ctnnnnccct	nncntaattn	ttctnnctan	540
ntcctanccn	cnnacnnncc	cancnatecn	nnnatacant	cnattnnntn	cnntcncntn	600
cncnnttcc	nnctnnnnc	tncncatnc	ccnnnannan	canntncccc	ncctnccctna	660
ccnncnncnc	cnccatccc	nnncnncnt	ccnnantnga	caannnnaat	cncnnnnncn	720
nnnnnnnnnn	tnnncnccn	gncnncnt	ncntcacnc	tnnncncta	nannnnntac	780
nnnacnnt	cctnnacnc	tncctnnng	antcncacna	ntnnnnnanc	nanaacnctn	840
tnnnnccata	atcccacacc	acnccntnc	ancntntnt	ncntctccc	ttcntatcnc	900
agctnnnnnt	nctntnnnnc	tncnccn	cnnactncnn	nnaccnncnn	cccantcagt	960
ccacntccn	cnnnnnnntn	nnncnancan	ctnnacnncn	cnantaacct	nnnnnacct	1020
tccc						1024

<210> 47

<211> 236

<212> DNA

<213> E. Coli

<400> 47

atatacacta	agtgaatgat	atcttccgat	ttatcttaat	cgtttatgga	taacggcaaa	60
gggcttcgtt	tttctctata	cttattcagc	actcacaaat	aaaggaacgc	caatgaaaat	120
tatactctgg	gctgtattga	ttattttcct	gattgggcta	ctggtagtga	ctggcgtatt	180
taagatgata	ttttaaaatt	aattaatgtc	atcagggtccg	aaaataacga	gaatat	236

<210> 48

<211> 418

<212> DNA

<213> E. Coli

<220>

<221> misc_feature

<222> (1)...(418)

<223> n = A,T,C or G

<400> 48

cggagattac	cgtgtgttgc	gatataTTTT	ttagtttcgc	gtggcaatac	atcagtggca	60
ataaaacgac	atatccagaa	aaatatacac	taagtgaatg	atatcttccg	attnatctta	120
ntcgtttatg	gataacggca	aagggttcg	ttttttccta	tacttattca	gcactcacia	180
ataaaggaac	gccaatgaaa	attatactct	ggcgtgtatt	gattattttc	ctgattgggc	240
tactggtggt	gactggcgta	tttaagatga	tatttttaaaa	ttaattaatg	tcatcaggtc	300
cgaataaac	gagaatattt	cagtctctca	tctgttgcg	ctcctgtcat	gtgcattgct	360
tcatataatc	actggcgcaa	ggagcgcgca	nggggcggcc	aatcgccgcc	ggccccctg	418

<210> 49

<211> 550

<212> DNA

<213> E. Coli

<400> 49
ctgctagtta cagggaaacac taatgacaga cagctaaaag ccctgtttta ttacgtatta 60
caaacagggg atgccagcg ttttcgtgca tttattgggt agatagcgga acgcgcacca 120
caagaaaagg agaaactgat gaccattgct gacagattac gtgaagaagg cgcaatgcag 180
ggcaaacacg aagaagccct gcgtattgct caggagatgc tggatagagg tttagacaga 240
gagttagtta tgatggtgac ccgactttca ccagacgatc ttatcgcgca aagccactaa 300
tctgttaaca ccgggagtta actggcggat gtttgctgta aaccacatca gcgaacgaca 360
tcgcgcagcg cctcttctaa atcgtaccag cgaaacgcaa aaccgccttc ttccagccgt 420
ttaggcagcg cgcgttgctc acctaatacc agtactgaag attcgcccat taacagtcga 480
atggcggtcg cggggacgcg caaaatggcc gggcgatgca gcgcatgacc gagcgcagtg 540
gcaaattggt 550

<210> 50
<211> 99
<212> DNA
<213> E. Coli

<400> 50
ttggcatctc ggtgttgccg atcttcatga tatccagccc gccggaaact tcttcccaaa 60
cggttttgct gttatccatt gagtcacgga actgccct 99

<210> 51
<211> 259
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(259)
<223> n = A,T,C or G

<400> 51
ccgtgccgag atgatcctgt naccatcatc cgttggtgaag tagtgattca cgacttcaag 60
gcgcttttca aaagggtatt ttggctttga catattaggg gctattccat ttcacgnc 120
aacaaaatgg gtgcagtaca tactcnttgg aaatcaacac aggaggctgg gaatgccga 180
gaaatataga ttactttctt taatagtgat ntgtttcacg cttttatttt tnaanaaagt 240
tnggcttact tcccgggn 259

<210> 52
<211> 877
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(877)
<223> n = A,T,C or G

<400> 52
cagcagagcg cggccttctt cgtcagattt cgcagtagtg gtaatggtaa tatccaaacc 60
acgaacgcgg tcgactttat cgtagtcgat ttctgggaag atgatctgct cagggacacc 120
catgctgtag ttaccacgac cgtcgaaaga cttagcggac aggccacgga agtcacggat 180
acgaggtaca gcaatagtga tcaggcgtc aaagaactcc cacatgcgtt cgccacgcag 240
agttacttta cagccgatcg gatagccctg acggattttg aagcctgcaa cagatttgcg 300
tgctttggtg atcagcgggt tttgaccgga gattgctgcc aggtctgctg ctgcgttatc 360
cagcagtttt ttgtcagcga tcgcttcacc aacacccatg ttcagggtga tcttctcgac 420
ccgagggact tgcagacag aattgtagtt aaactcagtc atgagttttt taactacttc 480

gtctttgtag	taatcatgca	gtttcgccat	cgtactactc	catgtcgggtg	aacgctctcc	540
tgagtaggac	aaatccgccg	ggagcggatt	tgaacgttgc	gaagcaacgg	cccggagggt	600
ggcgggcagg	acgcccgcga	taaactgcc	ggcatcaa	taagcagaag	gccatcctga	660
cggatggcct	ttttgcgttt	ctacaaactc	ttttggttat	ttttctaaat	cattcaaata	720
tgtatccgnt	catcccatcc	tatcgatgat	aagctgtcaa	acatgagaat	ttaatcaatc	780
taaagtttta	tggngttaaa	cttgggctgg	cagnttncca	atggcttaat	cagtngaggg	840
ccctatntta	acgaactngg	ctantttngg	tcaatcn			877

<210> 53
 <211> 291
 <212> DNA
 <213> E. Coli

<400> 53						
tgaacagcag	agatacggcc	agtgcggcca	atgttttttg	tccttttaa	ataacagagt	60
cctttaagga	tatagaatag	gggtatagct	acgccagaat	atcgatattg	attattgcta	120
gttttttagtt	ttgcttaaaa	atattgttag	ttttattaaa	tgcaaaaacta	aattattgggt	180
atcatgaatt	tgttgatga	tgaataaaat	ataggggggt	atagatagac	gtcattttca	240
taggggtata	aatgcgacta	ccatgaagtt	tttaattgaa	agtattgggt	t	291

<210> 54
 <211> 282
 <212> DNA
 <213> E. Coli

<400> 54						
ttattaaatg	caaaaactaaa	ttattggtat	catgaatttg	ttgtatgatg	aataaaatat	60
aggggggtat	agatagacgt	cattttcata	gggttataaa	tgcgactacc	atgaagtttt	120
taattgaaag	tattgggttg	ctgataat	gagctgttct	attcttttta	aatatctata	180
taggtctgtt	aatggatttt	atttttacaa	ttttttgtgt	ttaggcata	aaaaatcaac	240
cgcacatattg	aacggcgggt	taaaatattt	acaacttagc	aa		282

<210> 55
 <211> 293
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(293)
 <223> n = A,T,C or G

<400> 55						
cgggggtccgg	cgctcatcaa	caatcggggg	gcagcaaggg	gctgaaacgg	gaaagccct	60
cccgaagaag	gggccttgta	taaggaaagg	gttatgatga	agctcgatcat	catactgggt	120
gtgtngttac	tgttaagttt	cccgacttac	taacaactca	tcagaggggg	gagaaatcct	180
cccttaccct	tgttccttta	ctctaggttg	aaaaaacaac	agcgtcaata	ggcctgccat	240
gtacgaagcg	agatctgtga	accgctttcc	ggttagcctt	ttttatcctg	ttg	293

<210> 56
 <211> 300
 <212> DNA
 <213> E. Coli

<400> 56						
tctgcgttcc	gctaaaaggt	gcaaatgctc	aggacgttgc	agcgttttgc	gtgaccgctc	60
ggggaaggca	aaattgcctc	tgggaaagca	ttgcgcgggg	tccggcgctc	atcaacaatc	120

ggggggcagc	aaggggctga	aacgggaaa	cccccccca	agaaggggcc	ttgtataagg	180
aaagggttat	gatgaagctc	gtcatcatac	tggttggtgt	gttactgtta	agtttcccca	240
cttactaaca	actcatcaga	ggggggagaa	atcctccctt	acccttggtc	ctttactota	300

<210> 57
 <211> 359
 <212> DNA
 <213> E. Coli

<400> 57						
caacacagga	ggctgggaat	gccgcagaaa	tatagattac	tttctttaat	agtgatttgt	60
ttcacgcttt	tatttttcac	ctggatgata	agagattcac	tgtgtgaatt	gcatattaaa	120
caggagagtt	atgagctggc	ggcgttttta	gcctgcaa	tgaaagagta	agagtcttcg	180
gcgggaaatt	attccgcct	tacttacggc	gttgcgcatt	ctcattgcac	ccaaatttat	240
tcttcacaaa	aataataata	gattttatta	cgcgatcgat	tattttattc	ctgaaaacaa	300
ataaaaaaat	ccccgccaaa	tggcagggat	cttagattct	gtgcttttaa	gcagagatt	359

<210> 58
 <211> 700
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(700)
 <223> n = A,T,C or G

<400> 58						
aaaccttttt	ctcctgtttt	tcatagaggg	caacccatgt	cctgacctgg	gttcggggga	60
cacaaaaacg	tgccgagatg	atcctgtaac	catcatcagt	tgtgaagtag	tgattcacga	120
cttcaaggcg	cttttcaaaa	gggtattttg	gctttgacat	attaggggct	attccatttc	180
atcgccaac	aaaatgggtg	cagtacatac	tcgttgaaa	tcaacacagg	aggctgggaa	240
tgccgcagaa	atatagatta	ctttctttta	tagtgatttg	tttcacgctt	ttatttttca	300
cctggatgat	aagagattca	ctgtgtgaat	tgcatattaa	acaggagagt	tatgagctgg	360
cggcggtttt	agcctgcaaa	ttgaaagagt	aagagtcttc	ggcgggaaat	tattcccgcc	420
ttacttacgg	cggtgcgcac	tctcattgca	cccaaattta	ttcttcacaa	aaataataat	480
agattttatt	acgcgatcga	ttattttatt	cctgaaaaca	aataanaaaa	tccccgcaa	540
atggcaggga	tcttagattc	tgtgctttta	agcagagatt	acaggctggt	tacgttacca	600
gctgccgggc	ctttaacgcc	gctttcgatg	gtgaaggaca	ctttctgacc	ttcgtccaga	660
gattgtaacc	atcggtctgg	atagccnaga	aatgtccaac			700

<210> 59
 <211> 631
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(631)
 <223> n = A,T,C or G

<400> 59						
tggtggcatt	ggttgctgga	gagagaaaac	ccccgcacgt	tgagggtatg	cacctgacaa	60
caccacgggg	gctaattctg	actctagacc	actcaagaat	agccgcgaaa	cgttgtcatt	120
acaacacagg	cggtatatat	acgttcgcag	agctgggcat	ggccttctgg	catgatttag	180
cggctccggt	cattgctggc	attcttgcca	gtatgatcgt	gaactggctg	aacaagcgga	240
agtaacgtgt	catgcgggcg	tcaggctgcc	gtaatggcaa	tttgcgcccg	gaccaggccg	300

caggggggaa	actctgcggc	ctttttcggt	cttactgcgg	gtaaggcacc	cagtcgccgc	360
cgttcaggcg	aacgtacggt	ttatcctggt	attgaataac	tactgcattt	gagttctcgg	420
agaccggtgc	tgtttgtggc	aaccactggt	tgagtttttt	ccagtcaaca	ttgtcttcgg	480
tgaaaatott	gccatcgaga	acgcgaacca	ccagatcgga	gatagccagg	aagctgctcg	540
gttgttcgat	gacaatcggt	gccccctgat	gcggtgcctt	catgccgaag	aatttcaccc	600
caacggggac	gtcngtgata	gaccgggcta	g			631

<210> 60

<211> 648

<212> DNA

<213> E. Coli

<220>

<221> misc_feature

<222> (1)...(648)

<223> n = A,T,C or G

<400> 60

ggctcaggcn	tgctgattgt	ttttttgtgc	aatggcccng	tattagcgtc	gttgctgtcg	60
atggagagaa	tcataaacgt	ggtgaatgat	gattgttagc	aaggaaaact	gtcaaaaatc	120
ttcaaaaaat	ttgagggata	aggccggaat	ggctccggcc	agaggggaagt	taaccgcgaa	180
gctgttgctg	cttgaggggtc	gttttaacca	gacgccaggc	gctccatacg	ccaaaaccgc	240
gtctggccca	gcggaaccagc	atattaggat	ggcgaatcgt	ccagatcgcc	atcacgctac	300
tgccaaccag	cgcccaggag	cgcagactta	gcagcatatt	ccancgacga	tcgtaagcgc	360
ctgttgcttc	cagccattca	cgcagactgg	cggaagggnc	cgcgnetgac	caacttgnet	420
tttagtctga	tncanattan	attnataaac	gcagnanncn	ggtntgatta	atcntatttn	480
gctctngtct	ggtagttagc	nncggnnngt	ctcnttntna	cccnnttcnn	tttannttac	540
natnngtaan	ttatntttnt	nngtctnant	tntanttgng	tactntaagt	ntatncgnnn	600
atnntnnnan	nnnncagnnc	ntntttttta	aatntttnt	nanncnnc		648

<210> 61

<211> 737

<212> DNA

<213> E. Coli

<220>

<221> misc_feature

<222> (1)...(737)

<223> n = A,T,C or G

<400> 61

tgctaataatc	tttctcattg	agatgaaaat	taaggtaagc	gaggaaacac	accacaccat	60
aaacggaggc	aaataatgct	gggtaatatg	aatgttttta	tggccgtact	gggaataatt	120
ttattttctg	gtttttctggc	cgcgtatttc	agccacaaat	gggatgacta	atgaacggag	180
ataatccctc	acctaaccgg	ccccttggtta	cagttgtgta	caaggggcct	gatttttatg	240
acggcgaaaa	aaaaccgcca	gtaaaccggc	ggtgaatgct	tgcatggata	gatttgtgtt	300
ttgctttttac	gctaacaggc	attttctctgc	actgataacg	aatcgttgac	acagtagcat	360
cagttttctc	aatgaatggt	aaacggagct	taaactcggt	taatcacatt	ttgttcgtca	420
ataaacatgc	agcgatttct	tccggtttgc	ttaccctcat	acattgcccg	gtccgctctt	480
ccaatgacca	catccagagg	ctcttcagga	aatgcggagc	tcacacctgc	tgtcacggta	540
atgttgatat	gcccttcaga	atgtgtgatg	gcatggttat	cgactaactg	gcaaattctg	600
acacctgcac	gacatgcttc	ttcatcatta	gccgctttga	caataatgat	aaattcttcg	660
cccccgtagc	gataaaccgt	ttcgtaatna	cgcgtccaac	tgggntaagt	aaagttgcc	720
gggtgccgta	atcttac					737

<210> 62

<211> 648

<212> DNA
 <213> E. Coli
 <220>
 <221> misc_feature
 <222> (1)...(648)
 <223> n = A,T,C or G

<400> 62
 tgcttttgaa tatgtgctcg caatcttgag aaggaaatgg cgaccacgaa agaaaaggca 60
 aaaacgata atctgaaaga acccaagtat ttcagtataa gcattgaatg ccgaccagta 120
 aactctttcg gattcaccca gaaagtgaan ccaaaatgat aatcgtatac ataagtcttt 180
 cgagtggctc gtttagcaaaa agtttcaaca atggagtaaa tacatccaac atatcaataa 240
 ctctcaactg taaggggatt gaaatggtaa cccagctct tcgcttgagg ggtatagccg 300
 agaccaccga agccccggag gtggtgaaat aaaaccgggc acaacacgaa agggcgcat 360
 tccgatatcc ataaaagaag tcgggtcttt gtctggtaaa attaaattgg tgggaagtgc 420
 gcctccgggt tgtaaatacc gactttgctg ggtgtagcct ggcgcatca agtttttttc 480
 tggaagtctg ctgatgtccg ccttttttaa agggaatttt ggtgatgccg gtgaatgccg 540
 cttaaccccc cgtgggcccc gttaaaagtc atggttaagnc ctaatnggtt tggggtggga 600
 aaagccnact gnaaattggt tacctggttt gcaagtancc ctggaagg 648

<210> 63
 <211> 237
 <212> DNA
 <213> E. Coli
 <220>
 <221> misc_feature
 <222> (1)...(237)
 <223> n = A,T,C or G

<400> 63
 ggtgtttant tacaagagat tcattctttgt ntaaancccn gataagtaat tacgcataaa 60
 acaacaatga ttataatagc aaaaataaat attatcatct ttgatagatt acttgagata 120
 gccagcatct tgtaaagcct ttatcgtttt tttatgctct ggattaatat aatcactaca 180
 tctatctgag caatctgttg ttgatggaca tgtcaacca tggtcattta cagccaa 237

<210> 64
 <211> 427
 <212> DNA
 <213> E. Coli

<400> 64
 gataattaga gtttgctgctc agaaaattga cgttacccat aacaaatgaa aggccaggta 60
 aatcatgoca ttagtcattg ttgctatcgg tgtaatcttg ttgttgctcc tgatgatccg 120
 cttcaaaatg aacggcttca tcgctctcgt cctcgtggcg cttgctgttg gattaatgca 180
 aggaatgcgc ctggataaag ttattggctc catcaaagcc ggtgtcggcg ggacgctcgg 240
 tagccttgcc ctgatcatgg gttttggcgc aatgctggcg aaaatgctgg cagactgcgg 300
 tggcgacaaa cgtatcgcca ccacgctgat tgccaaattt ggtaaaaaac acatccagtg 360
 ggcggtggta ctgaccggtt ttaccgcttg ttttgccctg ttctatgaag tgggctttgt 420
 gctgatg 427

<210> 65
 <211> 261
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(261)
 <223> n = A,T,C or G

<400> 65

caaagaacct tcaacatgaa aaatatccat ttgtttgcaa aaaaagatta ttaggaagga	60
aattaatgca attatcgaaa attcaaaaaa tatccaaaaa tngtatactt tattccagaa	120
gagttcaata taatgtttgt cttcaatttt tcttacttca gggtaatata gattgctcat	180
tacattgtga gcttcacatt tatttaattt tctgttgact ccagctctcc gtgataacgg	240
ttttataatt agatgcttat c	261

<210> 66
 <211> 98
 <212> DNA
 <213> E. Coli

<400> 66

agatgattgc cgggaacttg ttagcggcac gcaggcggcg gctcgcaccc ttaccctgct	60
ctttacgtac ttctgcgttg atagtaaaca tttctttc	98

<210> 67
 <211> 260
 <212> DNA
 <213> E. Coli

<400> 67

aagcgcgaac gaagtcgatg tgctgcagct tcggtttgta cgggtgacgc tgtacgtcct	60
gagctttaac tttgatttct ttaccgtcaa caacgatggg cagaacttcg ctgtagaatt	120
cagcttttagc ttgcatgttc atgactttgt cgtgatccag ctcgatagcc agcggcgctt	180
ctttgccacc gtagatgatt gccgggaact tgttagcggc acgcaggcgg cggctcgcac	240
ccttaccctg ctctttacgt	260

<210> 68
 <211> 95
 <212> DNA
 <213> E. Coli

<400> 68

aaaaacggcg taaagaaagg ttgcaaacat gttaataaaa actcaaattg atcccacgta	60
tatattacgc cgcaaaatcc ttacaataaa caggg	95

<210> 69
 <211> 174
 <212> DNA
 <213> E. Coli

<400> 69

ttaattatta aaatagtgtg acgcgattat gtggttatgg gggtaaacad taaataaacc	60
agcggggagg ggaggtaaag tgaaaaaata aaaagcggat aatcttaata agcaggccgg	120
acagcatcgc catccggcac tgatacgagg tttatttcag ctcatcaacc atcg	174

<210> 70
 <211> 138
 <212> DNA
 <213> E. Coli

<400> 70
 agtctgtaaa aacgtcaaaa agagtgtttt atcaacagaa gaatggaggt ctgacagata 60
 gtagtaatgc aaaaaaatgg agacttaagt tgaatgaacg ggagtaaagc gaaaagacta 120
 tagagtgaag gagaaatt 138

<210> 71
 <211> 191
 <212> DNA
 <213> E. Coli

<400> 71
 tttgttggct taatattcta ttgttatctt tatttataga tgtttatatt gcatgaggtg 60
 gtttttggag agaagaatga ggaagatgcg tcgagccaca gaaacgttag ctttacctat 120
 agcggaggtg atgtgaattt aattttacaat agaaataatt tacatatcaa acagttagat 180
 gctttttgtc g 191

<210> 72
 <211> 244
 <212> DNA
 <213> E. Coli

<400> 72
 ggccatttat acaggaaaag cctatgtcag aacgtaaaaa ctcaaaatca cgccgtaatt 60
 atctcggttaa atgttcctgc ccaaactgca cccaagagtc agaacacagt ttttcaagag 120
 tacaaaaagg tgcccttttg atctgccctc attgcaacaa agtattccag acaaacttta 180
 aagctgtagc ctgattgatt ttattagtaa caagtatttt ttatatatta ataatatatt 240
 taaa 244

<210> 73
 <211> 327
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(327)
 <223> n = A,T,C or G

<400> 73
 aaattttcag gtaccttgtc accatacttt tttttctgag cattaatgat attttgagct 60
 tcttgaggat ctttaactcc ccacatttgg tggaaagtat tcatattaaa aggaaggntg 120
 aataatttgn ctttataaat cgccagtgga gaattagtaa aacgattaaa ttctactaaa 180
 tnattaaccg naaaaaaatt cccatatata tttatcattg gtatgaaaaa tatgtgcacc 240
 atatttatga atntggatac cctnacagtc ctctgtgtac gcatttccac cgatatgatt 300
 tcttttctna atcactaaaa cttttttt 327

<210> 74
 <211> 150
 <212> DNA
 <213> E. Coli

<400> 74
 gcagtgatcg aagcgatgac gaagtgtatg gaaaaatcag aaaaactcag caaatcctga 60
 tgacttttgcg cggacgtcag gccgccactt cgggtgcggtt acgtccgggt ttctttgctt 120
 tgtaaagcgc caaatctgcc gatttcaacc 150

<210> 75

<211> 330
 <212> DNA
 <213> E. Coli

<400> 75
 gaaagtatct tcggttattga catcactgga aaatataact tgcttttcat tattaaactc 60
 gaagcgcgta ccgatatctgg acaaacattt atcgagctta ccaaattcct gaagagggtt 120
 aactacagat aacattttgcg cgtcctttgc agtaatgccc gtcaaatacct tgacgggcat 180
 tatttagatt aaattaccag tatttcttcg gagtgaagaa tattaccagg tatatttaac 240
 acccacgttc gcggaaccagt cttgatctac gtcaccacca ccgaggtagt tagcatcggc 300
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 <213> E. Coli

<400> 76
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 gtaagctttt ttcc 194

<210> 77
 <211> 188
 <212> DNA
 <213> E. Coli

<400> 77
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 gttcttca 188

<210> 78
 <211> 173
 <212> DNA
 <213> E. Coli

<400> 78
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 gaaggattcg accactgcc a gttcttgcaa atcgtctttc acgcgattaa gca 173

<210> 79
 <211> 272
 <212> DNA
 <213> E. Coli

<220>
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 <222> (1)...(272)
 <223> n = A,T,C or G

<400> 79
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aaagaagaca ctactcttag ccctttaaca tttaacgcat tgtcacgaac tcttctgccg	180
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aacaccgata accattgagt tcagcagggc acgcgcggta ccagcctgtg cccaaccgtc	180
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<210> 81
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 <213> E. Coli

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 <212> DNA
 <213> E. Coli

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 <213> E. Coli

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 <212> DNA
 <213> E. Coli

<400> 84						
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<210> 85
 <211> 1761
 <212> DNA
 <213> E. Coli

<400> 85						
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<210> 86
 <211> 1185
 <212> DNA
 <213> E. Coli

<400> 86

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<210> 87
 <211> 2115
 <212> DNA
 <213> E. Coli

<400> 87

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 <211> 540
 <212> DNA
 <213> E. Coli

<400> 88

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<210> 89
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 <212> DNA
 <213> E. Coli

<400> 89

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 <211> 375
 <212> DNA
 <213> E. Coli

<400> 90						
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<210> 91
 <211> 366
 <212> DNA
 <213> E. Coli

<400> 91						
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<210> 92
 <211> 498
 <212> DNA
 <213> E. Coli

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 <211> 2145
 <212> DNA
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<400> 93

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<210> 94
 <211> 1767
 <212> DNA
 <213> E. Coli

<400> 94

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<210> 95
 <211> 1227
 <212> DNA
 <213> E. Coli

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<210> 96
 <211> 900
 <212> DNA
 <213> E. Coli

<400> 96

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<210> 97

<211> 771

<212> DNA

<213> E. Coli

<400> 97

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<210> 98

<211> 1335

<212> DNA

<213> E. Coli

<400> 98

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<210> 99
 <211> 1536
 <212> DNA
 <213> E. Coli

<400> 99

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<210> 100
 <211> 1029
 <212> DNA
 <213> E. Coli

<400> 100

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gccgcataa						1029

<210> 101
 <211> 993
 <212> DNA
 <213> E. Coli

<400> 101

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<210> 102
 <211> 1023
 <212> DNA
 <213> E. Coli

<400> 102

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<210> 103
 <211> 876
 <212> DNA
 <213> E. Coli

<400> 103

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catgccgatg tattaatgtg taogcgcggc attttgcgca gcgtagttcc ccctgcgacc	300
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<210> 104
 <211> 291
 <212> DNA
 <213> E. Coli

<400> 104

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gcagtggcgt tccataaaac cagcccccac taaaaaacct gtgtcgcgaa actggaatct	240
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<210> 105
 <211> 1152
 <212> DNA
 <213> E. Coli

<400> 105

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gcggtaaata ccgatgcaca agcgctgcgt aaaacagcgg ttggacagac gattcaaata	180
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<210> 106
 <211> 3048
 <212> DNA
 <213> E. Coli

<400> 106

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<210> 107
 <211> 885
 <212> DNA
 <213> E. Coli

<400> 107

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<210> 108
 <211> 654
 <212> DNA
 <213> E. Coli

<400> 108

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<210> 109
 <211> 261
 <212> DNA
 <213> E. Coli

<400> 109

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<210> 110
 <211> 1203
 <212> DNA
 <213> E. Coli

<400> 110						
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<210> 111
 <211> 1179
 <212> DNA
 <213> E. Coli

<400> 111						
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<400> 112

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 <211> 585
 <212> DNA
 <213> E. Coli

<400> 113

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 <211> 363
 <212> DNA
 <213> E. Coli

<400> 114

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 <212> DNA
 <213> E. Coli

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 <213> E. Coli

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 <211> 249
 <212> DNA
 <213> E. Coli

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 aaaagttaa 249

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 <211> 183
 <212> DNA
 <213> E. Coli

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 taa 183

<210> 119
 <211> 360
 <212> DNA
 <213> E. Coli

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 <211> 741
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 <213> E. Coli

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 <213> E. Coli

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<213> E. Coli

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<211> 720

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<213> E. Coli

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<211> 543

<212> DNA

<213> E. Coli

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 <212> DNA
 <213> E. Coli

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 <212> DNA
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<210> 132
 <211> 2223
 <212> DNA
 <213> E. Coli

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<211> 1059

<212> DNA

<213> E. Coli

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<213> E. Coli

<400> 147

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<213> E. Coli

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 <213> E. Coli

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<210> 151
 <211> 117
 <212> DNA
 <213> E. Coli

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<210> 152

<211> 1332
 <212> DNA
 <213> E. Coli

<400> 152

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 <212> DNA
 <213> E. Coli

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<210> 154
 <211> 180
 <212> DNA
 <213> E. Coli

<400> 154

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<210> 155
 <211> 504
 <212> DNA

<213> E. Coli

<400> 155

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<210> 156

<211> 354

<212> DNA

<213> E. Coli

<400> 156

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<210> 157

<211> 534

<212> DNA

<213> E. Coli

<400> 157

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<210> 158

<211> 393

<212> DNA

<213> E. Coli

<400> 158

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<210> 159

<211> 306
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<400> 159

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 <211> 540
 <212> DNA
 <213> E. Coli

<400> 160

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 <212> DNA
 <213> E. Coli

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<211> 1284
<212> DNA
<213> E. Coli

<400> 164

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<211> 1434
<212> DNA
<213> E. Coli

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<211> 1572
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<400> 170

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<211> 612
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 <213> E. Coli

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726

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<212> DNA
<213> E. Coli

<400> 204

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<213> E. Coli

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ccgggtaaac caaatagcgt gaatttttac gcccggtctaa tggcgacaca ggtgcctgtc 480
actgcggggc atatcaatgc cacggctacc ttcactcttg aatatcagta a 531

<210> 206
<211> 504
<212> DNA
<213> E. Coli

<400> 206
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<210> 207
<211> 903
<212> DNA
<213> E. Coli

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<212> DNA
<213> E. Coli

<400> 208

<210> 211
 <211> 291
 <212> DNA
 <213> E. Coli

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 tcggcgggta atgctggttt ctgggcattg cagttactcg ataaagtaac tccgtcacag 180
 tgggctgcaa tcggtgtgct gggtagcctg gtttttggcc tgctgacgta tctgacaaat 240
 ctttatttca agattaaaaga agacaggcgt aaggctgoga gaggagagta a 291

<210> 212
 <211> 216
 <212> DNA
 <213> E. Coli

<400> 212
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 aattatcgaa ctttatttga aggtcaaaaag gttacottct ctatagagag tgggtgctaaa 180
 ggtcctgcag cagcaaatgt catcattact gattaa 216

<210> 213
 <211> 1017
 <212> DNA
 <213> E. Coli

<400> 213
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<210> 215
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 <212> DNA
 <213> E. Coli

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 <211> 591
 <212> DNA
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<210> 217
 <211> 993
 <212> DNA
 <213> E. Coli

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 <212> DNA
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<210> 221
 <211> 1404
 <212> DNA
 <213> E. Coli

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 <211> 669
 <212> DNA
 <213> E. Coli

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<210> 223
 <211> 255
 <212> DNA
 <213> E. Coli

<400> 223						
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acgaccaaac	tgcacgtaca	tgacgagaac	aacgaatgcg	gtatcggtga	cgtgggtgaa	180
atccgcgaat	gccgtccgct	gtccaagact	aaatcctgga	cgctgggttcg	cgttgtagag	240
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<210> 224
 <211> 192
 <212> DNA
 <213> E. Coli

<400> 224						
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gcgggtgcgt	aa					192

<210> 225
 <211> 411
 <212> DNA

<213> E. Coli

<400> 225

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<210> 226

<211> 702

<212> DNA

<213> E. Coli

<400> 226

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tggatcttca	aaggcgagat	cctgggtggt	atggctgctg	ttgaacaacc	ggaaaaaccg	660
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<210> 227

<211> 333

<212> DNA

<213> E. Coli

<400> 227

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aagaaagcgg	ctgtactggt	caagaaagtt	ctggaatctg	ccattgctaa	cgctgaacac	180
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agcatgaagc	gcattatgcc	gcgtgcaaaa	ggtcgtgcag	atcgcatcct	gaagcgacc	300
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<210> 228

<211> 279

<212> DNA

<213> E. Coli

<400> 228

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tttcttaaca	tgatcggttt	gaccatcgct	gtccataatg	gtcgtcagca	cgttccggta	180
tttgtaaccg	acgaaatggt	tggtcacaaa	ctgggtgaat	tcgcaccgac	tcgtacttat	240
cgcggccacg	ctgctgataa	aaaagcgaag	aagaaataa			279

<210> 229

<211> 822

<212> DNA
<213> E. Coli

<400> 229

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<210> 230
<211> 303
<212> DNA
<213> E. Coli

<400> 230

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taa						303

<210> 231
<211> 630
<212> DNA
<213> E. Coli

<400> 231

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<210> 232
<211> 606
<212> DNA
<213> E. Coli

<400> 232

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gcatga						606

<210> 233
 <211> 312
 <212> DNA
 <213> E. Coli

<400> 233						
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<210> 234
 <211> 357
 <212> DNA
 <213> E. Coli

<400> 234						
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<210> 235
 <211> 198
 <212> DNA
 <213> E. Coli

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tgctgcgct	acgcataa					198

<210> 236
 <211> 543
 <212> DNA
 <213> E. Coli

<400> 236						
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 <212> DNA
 <213> E. Coli

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 <212> DNA
 <213> E. Coli

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 <211> 2904
 <212> DNA
 <213> E. Coli

<400> 239

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 <213> E. Coli

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<210> 241
 <211> 76
 <212> DNA
 <213> E. Coli

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<210> 242
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 <212> DNA
 <213> E. Coli

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<210> 243

<211> 221

<212> PRT

<213> E. Coli

<400> 243

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 20          25          30
Leu Pro Val Ser Ile Leu Gly Phe His Thr Thr Trp Gly Ala Phe Ser
 35          40          45
Phe Pro Phe Ile Phe Leu Ala Thr Asp Leu Thr Val Arg Ile Phe Gly
 50          55          60
Ala Pro Leu Ala Arg Arg Ile Ile Phe Ala Val Met Ile Pro Ala Leu
 65          70          75          80
Leu Ile Ser Tyr Val Ile Ser Ser Leu Phe Tyr Met Gly Ser Trp Gln
 85          90          95
Gly Phe Gly Ala Leu Ala His Phe Asn Leu Phe Val Ala Arg Ile Ala
 100         105         110
Thr Ala Ser Phe Met Ala Tyr Ala Leu Gly Gln Ile Leu Asp Val His
 115         120         125
Val Phe Asn Arg Leu Arg Gln Ser Arg Arg Trp Trp Leu Ala Pro Thr
 130         135         140
Ala Ser Thr Leu Phe Gly Asn Val Ser Asp Thr Leu Ala Phe Phe Phe
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Ile Ala Phe Trp Arg Ser Pro Asp Ala Phe Met Ala Glu His Trp Met
 165         170         175
Glu Ile Ala Leu Val Asp Tyr Cys Phe Lys Val Leu Ile Ser Ile Val
 180         185         190
Phe Phe Leu Pro Met Tyr Gly Val Leu Leu Asn Met Leu Leu Lys Arg
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<210> 244

<211> 203

<212> PRT

<213> E. Coli

<400> 244

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225					230					235					240		
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Pro	Glu	Ala	Asn	Leu	Val	Gly	Arg	Ala	Thr	Ala	Ile	Trp	Met	Ser	Phe		
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<210> 246
 <211> 586
 <212> PRT
 <213> E. Coli

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Leu	Leu	His	Thr	Arg	Ala	Ser	Ser	Ser	Phe	Met	Leu	Ala	Lys	Ala	Pro		
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Gln	Ser	Asp	Ala	Gly	Gln	Leu	Val	Gly	Gly	His	Tyr	Glu	Val	Ser	Gly		
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Thr	Asp	Ile	Glu	Arg	Lys	Ala	Glu	Leu	Gly	Gly	Asn	Ile	His	Ala	Lys
385					390					395					400
Gly	Met	Met	Ile	Met	Gln	Ala	Phe	Leu	Met	Ser	Glu	Leu	Gln	Leu	Glu
			405					410					415		
Gln	Gln	Ile	Pro	Phe	Ser	Ala	Ser	Leu	Thr	Phe	Glu	Gln	Ser	Tyr	Ser
			420					425					430		
Glu	Val	Asp	Gly	Asp	Ser	Ala	Ser	Met	Ala	Glu	Leu	Cys	Ala	Leu	Ile
		435					440					445			
Ser	Ala	Leu	Ala	Asp	Val	Pro	Val	Asn	Gln	Ser	Ile	Ala	Ile	Thr	Gly
	450					455					460				
Ser	Val	Asp	Gln	Phe	Gly	Arg	Ala	Gln	Pro	Val	Gly	Gly	Leu	Asn	Glu
465					470					475					480
Lys	Ile	Glu	Gly	Phe	Phe	Ala	Ile	Cys	Gln	Gln	Arg	Glu	Leu	Thr	Gly
			485					490					495		
Lys	Gln	Gly	Val	Ile	Ile	Pro	Thr	Ala	Asn	Val	Arg	His	Leu	Ser	Leu
			500					505					510		
His	Ser	Glu	Leu	Val	Lys	Ala	Val	Glu	Glu	Gly	Lys	Phe	Thr	Ile	Trp
		515					520					525			
Ala	Val	Asp	Asp	Val	Thr	Asp	Ala	Leu	Pro	Leu	Leu	Leu	Asn	Leu	Val
	530					535					540				
Trp	Asp	Gly	Glu	Gly	Gln	Thr	Thr	Leu	Met	Gln	Thr	Ile	Gln	Glu	Arg
545					550					555					560
Ile	Ala	Gln	Ala	Ser	Gln	Gln	Glu	Gly	Arg	His	Arg	Phe	Pro	Trp	Pro
			565					570					575		
Leu	Arg	Trp	Leu	Asn	Trp	Phe	Ile	Pro	Asn						
		580						585							

<210> 247
 <211> 394
 <212> PRT
 <213> E. Coli

<400> 247
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 Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Thr Ala Ala Ile
 20 25 30

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

Thr Thr Val Leu Ala Lys Thr Tyr Gly Gly Ala Ala Arg Ala Phe Asp
 35 40 45
 Gln Ile Asp Asn Ala Pro Glu Glu Lys Ala Arg Gly Ile Thr Ile Asn
 50 55 60
 Thr Ser His Val Glu Tyr Asp Thr Pro Thr Arg His Tyr Ala His Val
 65 70 75 80
 Asp Cys Pro Gly His Ala Asp Tyr Val Lys Asn Met Ile Thr Gly Ala
 85 90 95
 Ala Gln Met Asp Gly Ala Ile Leu Val Val Ala Ala Thr Asp Gly Pro
 100 105 110
 Met Pro Gln Thr Arg Glu His Ile Leu Leu Gly Arg Gln Val Gly Val
 115 120 125
 Pro Tyr Ile Ile Val Phe Leu Asn Lys Cys Asp Met Val Asp Asp Glu
 130 135 140
 Glu Leu Leu Glu Leu Val Glu Met Glu Val Arg Glu Leu Leu Ser Gln
 145 150 155 160
 Tyr Asp Phe Pro Gly Asp Asp Thr Pro Ile Val Arg Gly Ser Ala Leu
 165 170 175
 Lys Ala Leu Glu Gly Asp Ala Glu Trp Glu Ala Lys Ile Leu Glu Leu
 180 185 190
 Ala Gly Phe Leu Asp Ser Tyr Ile Pro Glu Pro Glu Arg Ala Ile Asp
 195 200 205
 Lys Pro Phe Leu Leu Pro Ile Glu Asp Val Phe Ser Ile Ser Gly Arg
 210 215 220
 Gly Thr Val Val Thr Gly Arg Val Glu Arg Gly Ile Ile Lys Val Gly
 225 230 235 240
 Glu Glu Val Glu Ile Val Gly Ile Lys Glu Thr Gln Lys Ser Thr Cys
 245 250 255
 Thr Gly Val Glu Met Phe Arg Lys Leu Leu Asp Glu Gly Arg Ala Gly
 260 265 270
 Glu Asn Val Gly Val Leu Leu Arg Gly Ile Lys Arg Glu Glu Ile Glu
 275 280 285
 Arg Gly Gln Val Leu Ala Lys Pro Gly Thr Ile Lys Pro His Thr Lys
 290 295 300
 Phe Glu Ser Glu Val Tyr Ile Leu Ser Lys Asp Glu Gly Gly Arg His
 305 310 315 320
 Thr Pro Phe Phe Lys Gly Tyr Arg Pro Gln Phe Tyr Phe Arg Thr Thr
 325 330 335
 Asp Val Thr Gly Thr Ile Glu Leu Pro Glu Gly Val Glu Met Val Met
 340 345 350
 Pro Gly Asp Asn Ile Lys Met Val Val Thr Leu Ile His Pro Ile Ala
 355 360 365
 Met Asp Asp Gly Leu Arg Phe Ala Ile Arg Glu Gly Gly Arg Thr Val
 370 375 380
 Gly Ala Gly Val Val Ala Lys Val Leu Gly
 385 390

<210> 248
 <211> 704
 <212> PRT
 <213> E. Coli

<400> 248
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Ala Asn Val Gly Lys	Pro Gln Val Ala Tyr Arg Glu Thr Ile Arg Gln					
	485		490		495	
Lys Val Thr Asp Val Glu Gly Lys His Ala Lys Gln Ser Gly Gly Arg						
	500		505		510	
Gly Gln Tyr Gly His Val Val Ile Asp Met Tyr Pro Leu Glu Pro Gly						
	515		520		525	
Ser Asn Pro Lys Gly Tyr Glu Phe Ile Asn Asp Ile Lys Gly Gly Val						
	530		535		540	
Ile Pro Gly Glu Tyr Ile Pro Ala Val Asp Lys Gly Ile Gln Glu Gln						
	545		550		555	
Leu Lys Ala Gly Pro Leu Ala Gly Tyr Pro Val Val Asp Met Gly Ile						
	565		570		575	
Arg Leu His Phe Gly Ser Tyr His Asp Val Asp Ser Ser Glu Leu Ala						
	580		585		590	
Phe Lys Leu Ala Ala Ser Ile Ala Phe Lys Glu Gly Phe Lys Lys Ala						
	595		600		605	
Lys Pro Val Leu Leu Glu Pro Ile Met Lys Val Glu Val Glu Thr Pro						
	610		615		620	
Glu Glu Asn Thr Gly Asp Val Ile Gly Asp Leu Ser Arg Arg Arg Gly						
	625		630		635	
Met Leu Lys Gly Gln Glu Ser Glu Val Thr Gly Val Lys Ile His Ala						
	645		650		655	
Glu Val Pro Leu Ser Glu Met Phe Gly Tyr Ala Thr Gln Leu Arg Ser						
	660		665		670	
Leu Thr Lys Gly Arg Ala Ser Tyr Thr Met Glu Phe Leu Lys Tyr Asp						
	675		680		685	
Glu Ala Pro Ser Asn Val Ala Gln Ala Val Ile Glu Ala Arg Gly Lys						
	690		695		700	

<210> 249
 <211> 179
 <212> PRT
 <213> E. Coli

<400> 249

Met Pro Arg Arg Arg Val Ile Gly Gln Arg Lys Ile Leu Pro Asp Pro														
1		5		10		15								
Lys Phe Gly Ser Glu Leu Leu Ala Lys Phe Val Asn Ile Leu Met Val														
	20		25		30									
Asp Gly Lys Lys Ser Thr Ala Glu Ser Ile Val Tyr Ser Ala Leu Glu														
	35		40		45									
Thr Leu Ala Gln Arg Ser Gly Lys Ser Glu Leu Glu Ala Phe Glu Val														
	50		55		60									
Ala Leu Glu Asn Val Arg Pro Thr Val Glu Val Lys Ser Arg Arg Val														
	65		70		75									
Gly Gly Ser Thr Tyr Gln Val Pro Val Glu Val Arg Pro Val Arg Arg														
	85		90		95									
Asn Ala Leu Ala Met Arg Trp Ile Val Glu Ala Ala Arg Lys Arg Gly														
	100		105		110									
Asp Lys Ser Met Ala Leu Arg Leu Ala Asn Glu Leu Ser Asp Ala Ala														
	115		120		125									
Glu Asn Lys Gly Thr Ala Val Lys Lys Arg Glu Asp Val His Arg Met														
	130		135		140									
Ala Glu Ala Asn Lys Ala Phe Ala His Tyr Arg Trp Leu Ser Leu Arg														
	145		150		155									

Ser Phe Ser His Gln Ala Gly Ala Ser Ser Lys Gln Pro Ala Leu Gly
165 170 175
Tyr Leu Asn

<210> 250
<211> 124
<212> PRT
<213> E. Coli

<400> 250
Met Ala Thr Val Asn Gln Leu Val Arg Lys Pro Arg Ala Arg Lys Val
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Ala Lys Ser Asn Val Pro Ala Leu Glu Ala Cys Pro Gln Lys Arg Gly
20 25 30
Val Cys Thr Arg Val Tyr Thr Thr Thr Pro Lys Lys Pro Asn Ser Ala
35 40 45
Leu Arg Lys Val Cys Arg Val Arg Leu Thr Asn Gly Phe Glu Val Thr
50 55 60
Ser Tyr Ile Gly Gly Glu Gly His Asn Leu Gln Glu His Ser Val Ile
65 70 75 80
Leu Ile Arg Gly Gly Arg Val Lys Asp Leu Pro Gly Val Arg Tyr His
85 90 95
Thr Val Arg Gly Ala Leu Asp Cys Ser Gly Val Lys Asp Arg Lys Gln
100 105 110
Ala Arg Ser Lys Tyr Gly Val Lys Arg Pro Lys Ala
115 120

<210> 251
<211> 165
<212> PRT
<213> E. Coli

<400> 251
Met Ala Leu Asn Leu Gln Asp Lys Gln Ala Ile Val Ala Glu Val Ser
1 5 10 15
Glu Val Ala Lys Gly Ala Leu Ser Ala Val Val Ala Asp Ser Arg Gly
20 25 30
Val Thr Val Asp Lys Met Thr Glu Leu Arg Lys Ala Gly Arg Glu Ala
35 40 45
Gly Val Tyr Met Arg Val Val Arg Asn Thr Leu Leu Arg Arg Ala Val
50 55 60
Glu Gly Thr Pro Phe Glu Cys Leu Lys Asp Ala Phe Val Gly Pro Thr
65 70 75 80
Leu Ile Ala Tyr Ser Met Glu His Pro Gly Ala Ala Ala Arg Leu Phe
85 90 95
Lys Glu Phe Ala Lys Ala Asn Ala Lys Phe Glu Val Lys Ala Ala Ala
100 105 110
Phe Glu Gly Glu Leu Ile Pro Ala Ser Gln Ile Asp Arg Leu Ala Thr
115 120 125
Leu Pro Thr Tyr Glu Glu Ala Ile Ala Arg Leu Met Ala Thr Met Lys
130 135 140
Glu Ala Ser Ala Gly Lys Leu Val Arg Thr Leu Ala Ala Val Arg Asp
145 150 155 160
Ala Lys Glu Ala Ala

<210> 252
 <211> 121
 <212> PRT
 <213> E. Coli

<400> 252

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Met Ser Ile Thr Lys Asp Gln Ile Ile Glu Ala Val Ala Ala Met Ser
 1           5           10           15
Val Met Asp Val Val Glu Leu Ile Ser Ala Met Glu Glu Lys Phe Gly
      20           25           30
Val Ser Ala Ala Ala Val Ala Val Ala Ala Gly Pro Val Glu Ala
      35           40           45
Ala Glu Glu Lys Thr Glu Phe Asp Val Ile Leu Lys Ala Ala Gly Ala
      50           55           60
Asn Lys Val Ala Val Ile Lys Ala Val Arg Gly Ala Thr Gly Leu Gly
      65           70           75           80
Leu Lys Glu Ala Lys Asp Leu Val Glu Ser Ala Pro Ala Ala Leu Lys
      85           90           95
Glu Gly Val Ser Lys Asp Asp Ala Glu Ala Leu Lys Lys Ala Leu Glu
      100          105          110
Glu Ala Gly Ala Glu Val Glu Val Lys
      115          120

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<210> 253
 <211> 714
 <212> PRT
 <213> E. Coli

<400> 253

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Met Ser Arg Ile Ile Met Leu Ile Pro Thr Gly Thr Ser Val Gly Leu
 1           5           10           15
Thr Ser Val Ser Leu Gly Val Ile Arg Ala Met Glu Arg Lys Gly Val
      20           25           30
Arg Leu Ser Val Phe Lys Pro Ile Ala Gln Pro Arg Thr Gly Gly Asp
      35           40           45
Ala Pro Asp Gln Thr Thr Thr Ile Val Arg Ala Asn Ser Ser Thr Thr
      50           55           60
Thr Ala Ala Glu Pro Leu Lys Met Ser Tyr Val Glu Gly Leu Leu Ser
      65           70           75           80
Ser Asn Gln Lys Asp Val Leu Met Glu Glu Ile Val Ala Asn Tyr His
      85           90           95
Ala Asn Thr Lys Asp Ala Glu Val Val Leu Val Glu Gly Leu Val Pro
      100          105          110
Thr Arg Lys His Gln Phe Ala Gln Ser Leu Asn Tyr Glu Ile Ala Lys
      115          120          125
Thr Leu Asn Ala Glu Ile Val Phe Val Met Ser Gln Gly Thr Asp Thr
      130          135          140
Pro Glu Gln Leu Lys Glu Arg Ile Glu Leu Thr Arg Asn Ser Phe Gly
      145          150          155          160
Gly Ala Lys Asn Thr Asn Ile Thr Gly Val Ile Val Asn Lys Leu Asn
      165          170          175
Ala Pro Val Asp Glu Gln Gly Arg Thr Arg Pro Asp Leu Ser Glu Ile
      180          185          190

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Phe Asp Asp Ser Ser Lys Ala Lys Val Asn Asn Val Asp Pro Ala Lys
 195 200 205
 Leu Gln Glu Ser Ser Pro Leu Pro Val Leu Gly Ala Val Pro Trp Ser
 210 215 220
 Phe Asp Leu Ile Ala Thr Arg Ala Ile Asp Met Ala Arg His Leu Asn
 225 230 235 240
 Ala Thr Ile Ile Asn Glu Gly Asp Ile Asn Thr Arg Arg Val Lys Ser
 245 250 255
 Val Thr Phe Cys Ala Arg Ser Ile Pro His Met Leu Glu His Phe Arg
 260 265 270
 Ala Gly Ser Leu Leu Val Thr Ser Ala Asp Arg Pro Asp Val Leu Val
 275 280 285
 Ala Ala Cys Leu Ala Ala Met Asn Gly Val Glu Ile Gly Ala Leu Leu
 290 295 300
 Leu Thr Gly Gly Tyr Glu Met Asp Ala Arg Ile Ser Lys Leu Cys Glu
 305 310 315 320
 Arg Ala Phe Ala Thr Gly Leu Pro Val Phe Met Val Asn Thr Asn Thr
 325 330 335
 Trp Gln Thr Ser Leu Ser Leu Gln Ser Phe Asn Leu Glu Val Pro Val
 340 345 350
 Asp Asp His Glu Arg Ile Glu Lys Val Gln Glu Tyr Val Ala Asn Tyr
 355 360 365
 Ile Asn Ala Asp Trp Ile Glu Ser Leu Thr Ala Thr Ser Glu Arg Ser
 370 375 380
 Arg Arg Leu Ser Pro Pro Ala Phe Arg Tyr Gln Leu Thr Glu Leu Ala
 385 390 395 400
 Arg Lys Ala Gly Lys Arg Ile Val Leu Pro Glu Gly Asp Glu Pro Arg
 405 410 415
 Thr Val Lys Ala Ala Ala Ile Cys Ala Glu Arg Gly Ile Ala Thr Cys
 420 425 430
 Val Leu Leu Gly Asn Pro Ala Glu Ile Asn Arg Val Ala Ala Ser Gln
 435 440 445
 Gly Val Glu Leu Gly Ala Gly Ile Glu Ile Val Asp Pro Glu Val Val
 450 455 460
 Arg Glu Ser Tyr Val Gly Arg Leu Val Glu Leu Arg Lys Asn Lys Gly
 465 470 475 480
 Met Thr Glu Thr Val Ala Arg Glu Gln Leu Glu Asp Asn Val Val Leu
 485 490 495
 Gly Thr Leu Met Leu Glu Gln Asp Glu Val Asp Gly Leu Val Ser Gly
 500 505 510
 Ala Val His Thr Thr Ala Asn Thr Ile Arg Pro Pro Leu Gln Leu Ile
 515 520 525
 Lys Thr Ala Pro Gly Ser Ser Leu Val Ser Ser Val Phe Phe Met Leu
 530 535 540
 Leu Pro Glu Gln Val Tyr Val Tyr Gly Asp Cys Ala Ile Asn Pro Asp
 545 550 555 560
 Pro Thr Ala Glu Gln Leu Ala Glu Ile Ala Ile Gln Ser Ala Asp Ser
 565 570 575
 Ala Ala Ala Phe Gly Ile Glu Pro Arg Val Ala Met Leu Ser Tyr Ser
 580 585 590
 Thr Gly Thr Ser Gly Ala Gly Ser Asp Val Glu Lys Val Arg Glu Ala
 595 600 605
 Thr Arg Leu Ala Gln Glu Lys Arg Pro Asp Leu Met Ile Asp Gly Pro
 610 615 620
 Leu Gln Tyr Asp Ala Ala Val Met Ala Asp Val Ala Lys Ser Lys Ala
 625 630 635 640
 Pro Asn Ser Pro Val Ala Gly Arg Ala Thr Val Phe Ile Phe Pro Asp

				645					650					655			
Leu	Asn	Thr	Gly	Asn	Thr	Thr	Tyr	Lys	Ala	Val	Gln	Arg	Ser	Ala	Asp		
			660					665					670				
Leu	Ile	Ser	Ile	Gly	Pro	Met	Leu	Gln	Gly	Met	Arg	Lys	Pro	Val	Asn		
		675					680					685					
Asp	Leu	Ser	Arg	Gly	Ala	Leu	Val	Asp	Asp	Ile	Val	Tyr	Thr	Ile	Ala		
	690					695					700						
Leu	Thr	Ala	Ile	Gln	Ser	Ala	Gln	Gln	Gln								
705					710												

<210> 254
 <211> 588
 <212> PRT
 <213> E. Coli

Met	Asn	Asn	Ser	Ile	Asn	His	Lys	Phe	His	His	Ile	Ser	Arg	Ala	Glu		
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Tyr	Gln	Glu	Leu	Leu	Ala	Val	Ser	Arg	Gly	Asp	Ala	Val	Ala	Asp	Tyr		
			20					25					30				
Ile	Ile	Asp	Asn	Val	Ser	Ile	Leu	Asp	Leu	Ile	Asn	Gly	Gly	Glu	Ile		
		35					40					45					
Ser	Gly	Pro	Ile	Val	Ile	Lys	Gly	Arg	Tyr	Ile	Ala	Gly	Val	Gly	Ala		
	50					55					60						
Glu	Tyr	Thr	Asp	Ala	Pro	Ala	Leu	Gln	Arg	Ile	Asp	Ala	Arg	Gly	Ala		
65					70					75					80		
Thr	Ala	Val	Pro	Gly	Phe	Ile	Asp	Ala	His	Leu	His	Ile	Glu	Ser	Ser		
			85						90					95			
Met	Met	Thr	Pro	Val	Thr	Phe	Glu	Thr	Ala	Thr	Leu	Pro	Arg	Gly	Leu		
			100					105						110			
Thr	Thr	Val	Ile	Cys	Asp	Pro	His	Glu	Ile	Val	Asn	Val	Met	Gly	Glu		
		115					120						125				
Ala	Gly	Phe	Ala	Trp	Phe	Ala	Arg	Cys	Ala	Glu	Gln	Ala	Arg	Gln	Asn		
	130					135						140					
Gln	Tyr	Leu	Gln	Val	Ser	Ser	Cys	Val	Pro	Ala	Leu	Glu	Gly	Cys	Asp		
145					150					155					160		
Val	Asn	Gly	Ala	Ser	Phe	Thr	Leu	Glu	Gln	Met	Leu	Ala	Trp	Arg	Asp		
			165						170					175			
His	Pro	Gln	Val	Thr	Gly	Leu	Ala	Glu	Met	Met	Asp	Tyr	Pro	Gly	Val		
		180						185					190				
Ile	Ser	Gly	Gln	Asn	Ala	Leu	Leu	Asp	Lys	Leu	Asp	Ala	Phe	Arg	His		
	195						200					205					
Leu	Thr	Leu	Asp	Gly	His	Cys	Pro	Gly	Leu	Gly	Gly	Lys	Glu	Leu	Asn		
	210					215						220					
Ala	Tyr	Ile	Thr	Ala	Gly	Ile	Glu	Asn	Cys	His	Glu	Ser	Tyr	Gln	Leu		
225					230					235					240		
Glu	Glu	Gly	Arg	Arg	Lys	Leu	Gln	Leu	Gly	Met	Ser	Leu	Met	Ile	Arg		
			245						250					255			
Glu	Gly	Ser	Ala	Ala	Arg	Asn	Leu	Asn	Ala	Leu	Ala	Pro	Leu	Ile	Asn		
			260					265					270				
Glu	Phe	Asn	Ser	Pro	Gln	Cys	Met	Leu	Cys	Thr	Asp	Asp	Arg	Asn	Pro		
	275						280					285					
Trp	Glu	Ile	Ala	His	Glu	Gly	His	Ile	Asp	Ala	Leu	Ile	Arg	Arg	Leu		
	290					295					300						
Ile	Glu	Gln	His	Asn	Val	Pro	Leu	His	Val	Ala	Tyr	Arg	Val	Ala	Ser		
305					310					315					320		

Trp Ser Thr Ala Arg His Phe Gly Leu Asn His Leu Gly Leu Leu Ala
 325 330 335
 Pro Gly Lys Gln Ala Asp Ile Val Leu Leu Ser Asp Ala Arg Lys Val
 340 345 350
 Thr Val Gln Gln Val Leu Val Lys Gly Glu Pro Ile Asp Ala Gln Thr
 355 360 365
 Leu Gln Ala Glu Glu Ser Ala Arg Leu Ala Gln Ser Ala Pro Pro Tyr
 370 375 380
 Gly Asn Thr Ile Ala Arg Gln Pro Val Ser Ala Ser Asp Phe Ala Leu
 385 390 395 400
 Gln Phe Thr Pro Gly Lys Arg Tyr Arg Val Ile Asp Val Ile His Asn
 405 410 415
 Glu Leu Ile Thr His Ser His Ser Ser Val Tyr Ser Glu Asn Gly Phe
 420 425 430
 Asp Arg Asp Asp Val Ser Phe Ile Ala Val Leu Glu Arg Tyr Gly Gln
 435 440 445
 Arg Leu Ala Pro Ala Cys Gly Leu Leu Gly Gly Phe Gly Leu Asn Glu
 450 455 460
 Gly Ala Leu Ala Ala Thr Val Ser His Asp Ser His Asn Ile Val Val
 465 470 475 480
 Ile Gly Arg Ser Ala Glu Glu Met Ala Leu Ala Val Asn Gln Val Ile
 485 490 495
 Gln Asp Gly Gly Gly Leu Cys Val Val Arg Asn Gly Gln Val Gln Ser
 500 505 510
 His Leu Pro Leu Pro Ile Ala Gly Leu Met Ser Thr Asp Thr Ala Gln
 515 520 525
 Ser Leu Ala Glu Gln Ile Asp Ala Leu Lys Ala Ala Arg Glu Cys
 530 535 540
 Gly Pro Leu Pro Asp Glu Pro Phe Ile Gln Met Ala Phe Leu Ser Leu
 545 550 555 560
 Pro Val Ile Pro Ala Leu Lys Leu Thr Ser Gln Gly Leu Phe Asp Gly
 565 570 575
 Glu Lys Phe Ala Phe Thr Thr Leu Glu Val Thr Glu
 580 585

<210> 255
 <211> 408
 <212> PRT
 <213> E. Coli

<400> 255
 Met Ala Tyr Cys Asn Pro Gly Leu Glu Ser Arg Pro Asn Lys Arg Asn
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 Ala Leu Arg Arg His Val Val Thr Gly Ile Gly Met Lys Ile Val Ile
 20 25 30
 Ala Pro Asp Ser Tyr Lys Glu Ser Leu Ser Ala Ser Glu Val Ala Gln
 35 40 45
 Ala Ile Glu Lys Gly Phe Arg Glu Ile Phe Pro Asp Ala Gln Tyr Val
 50 55 60
 Ser Val Pro Val Ala Asp Gly Gly Glu Gly Thr Val Glu Ala Met Ile
 65 70 75 80
 Ala Ala Thr Gln Gly Ala Glu Arg His Ala Trp Val Thr Gly Pro Leu
 85 90 95
 Gly Glu Lys Val Asn Ala Ser Trp Gly Ile Ser Gly Asp Gly Lys Thr
 100 105 110
 Ala Phe Ile Glu Met Ala Ala Ala Ser Gly Leu Glu Leu Val Pro Ala

	115		120		125										
Glu	Lys	Arg	Asp	Pro	Leu	Val	Thr	Thr	Ser	Arg	Gly	Thr	Gly	Glu	Leu
	130					135					140				
Ile	Leu	Gln	Ala	Leu	Glu	Ser	Gly	Ala	Thr	Asn	Ile	Ile	Ile	Gly	Ile
145					150					155					160
Gly	Gly	Ser	Ala	Thr	Asn	Asp	Gly	Gly	Ala	Gly	Met	Val	Gln	Ala	Leu
				165					170					175	
Gly	Ala	Lys	Leu	Cys	Asp	Ala	Asn	Gly	Asn	Glu	Ile	Gly	Phe	Gly	Gly
			180					185					190		
Gly	Ser	Leu	Asn	Thr	Leu	Asn	Asp	Ile	Asp	Ile	Ser	Gly	Leu	Asp	Pro
	195						200					205			
Arg	Leu	Lys	Asp	Cys	Val	Ile	Arg	Val	Ala	Cys	Asp	Val	Thr	Asn	Pro
	210					215					220				
Leu	Val	Gly	Asp	Asn	Gly	Ala	Ser	Arg	Ile	Phe	Gly	Pro	Gln	Lys	Gly
225					230					235					240
Ala	Ser	Glu	Ala	Met	Ile	Val	Glu	Leu	Asp	Asn	Asn	Leu	Ser	His	Tyr
				245					250					255	
Ala	Glu	Val	Ile	Lys	Lys	Ala	Leu	His	Val	Asp	Val	Lys	Asp	Val	Pro
			260					265					270		
Gly	Ala	Gly	Ala	Ala	Gly	Gly	Met	Gly	Ala	Ala	Leu	Met	Ala	Phe	Leu
	275						280					285			
Gly	Ala	Glu	Leu	Lys	Ser	Gly	Ile	Glu	Ile	Val	Thr	Thr	Ala	Leu	Asn
	290					295					300				
Leu	Glu	Glu	His	Ile	His	Asp	Cys	Thr	Leu	Val	Ile	Thr	Gly	Glu	Gly
305					310					315					320
Arg	Ile	Asp	Ser	Gln	Ser	Ile	His	Gly	Lys	Val	Pro	Ile	Gly	Val	Ala
				325					330					335	
Asn	Val	Ala	Lys	Lys	Tyr	His	Lys	Pro	Val	Ile	Gly	Ile	Ala	Gly	Ser
			340					345					350		
Leu	Thr	Asp	Asp	Val	Gly	Val	Val	His	Gln	His	Gly	Ile	Asp	Ala	Val
		355					360					365			
Phe	Ser	Val	Leu	Thr	Ser	Ile	Gly	Thr	Leu	Asp	Glu	Ala	Phe	Arg	Gly
	370					375					380				
Ala	Tyr	Asp	Asn	Ile	Cys	Arg	Ala	Ser	Arg	Asn	Ile	Ala	Ala	Thr	Leu
385					390					395					400
Ala	Ile	Gly	Met	Arg	Asn	Ala	Gly								
				405											

<210> 256
 <211> 299
 <212> PRT
 <213> E. Coli

<400> 256															
Met	Ile	Asp	Met	Thr	Met	Lys	Val	Gly	Phe	Ile	Gly	Leu	Gly	Ile	Met
1				5					10					15	
Gly	Lys	Pro	Met	Ser	Lys	Asn	Leu	Leu	Lys	Ala	Gly	Tyr	Ser	Leu	Val
			20					25				30			
Val	Ala	Asp	Arg	Asn	Pro	Glu	Ala	Ile	Ala	Asp	Val	Ile	Ala	Ala	Gly
		35					40					45			
Ala	Glu	Thr	Ala	Ser	Thr	Ala	Lys	Ala	Ile	Ala	Glu	Gln	Cys	Asp	Val
	50					55					60				
Ile	Ile	Thr	Met	Leu	Pro	Asn	Ser	Pro	His	Val	Lys	Glu	Val	Ala	Leu
65					70				75						80
Gly	Glu	Asn	Gly	Ile	Ile	Glu	Gly	Ala	Lys	Pro	Gly	Thr	Val	Leu	Ile
				85					90					95	

Asp	Met	Ser	Ser	Ile	Ala	Pro	Leu	Ala	Ser	Arg	Glu	Ile	Ser	Glu	Ala	
			100					105					110			
Leu	Lys	Ala	Lys	Gly	Ile	Asp	Met	Leu	Asp	Ala	Pro	Val	Ser	Gly	Gly	
		115					120					125				
Glu	Pro	Lys	Ala	Ile	Asp	Gly	Thr	Leu	Ser	Val	Met	Val	Gly	Gly	Asp	
	130					135					140					
Lys	Ala	Ile	Phe	Asp	Lys	Tyr	Tyr	Asp	Leu	Met	Lys	Ala	Met	Ala	Gly	
145					150					155					160	
Ser	Val	Val	His	Thr	Gly	Glu	Ile	Gly	Ala	Gly	Asn	Val	Thr	Lys	Leu	
			165						170					175		
Ala	Asn	Gln	Val	Ile	Val	Ala	Leu	Asn	Ile	Ala	Ala	Met	Ser	Glu	Ala	
		180						185					190			
Leu	Thr	Leu	Ala	Thr	Lys	Ala	Gly	Val	Asn	Pro	Asp	Leu	Val	Tyr	Gln	
		195					200					205				
Ala	Ile	Arg	Gly	Gly	Leu	Ala	Gly	Ser	Thr	Val	Leu	Asp	Ala	Lys	Ala	
	210					215					220					
Pro	Met	Val	Met	Asp	Arg	Asn	Phe	Lys	Pro	Gly	Phe	Arg	Ile	Asp	Leu	
225					230					235					240	
His	Ile	Lys	Asp	Leu	Ala	Asn	Ala	Leu	Asp	Thr	Ser	His	Gly	Val	Gly	
			245						250					255		
Ala	Gln	Leu	Pro	Leu	Thr	Ala	Ala	Val	Met	Glu	Met	Met	Gln	Ala	Leu	
		260						265					270			
Arg	Ala	Asp	Gly	Leu	Gly	Thr	Ala	Asp	His	Ser	Ala	Leu	Ala	Cys	Tyr	
	275						280					285				
Tyr	Glu	Lys	Leu	Ala	Lys	Val	Glu	Val	Thr	Arg						
	290					295										

<210> 257
 <211> 256
 <212> PRT
 <213> E. Coli

<400> 257

Met	Asn	Asn	Asp	Val	Phe	Pro	Asn	Lys	Phe	Lys	Ala	Ala	Leu	Ala	Ala	
1				5					10					15		
Lys	Gln	Val	Gln	Ile	Gly	Cys	Trp	Ser	Ala	Leu	Ser	Asn	Pro	Ile	Ser	
		20					25						30			
Thr	Glu	Val	Leu	Gly	Leu	Ala	Gly	Phe	Asp	Trp	Leu	Val	Leu	Asp	Gly	
	35						40					45				
Glu	His	Ala	Pro	Asn	Asp	Ile	Ser	Thr	Phe	Ile	Pro	Gln	Leu	Met	Ala	
	50				55						60					
Leu	Lys	Gly	Ser	Ala	Ser	Ala	Pro	Val	Val	Arg	Val	Pro	Thr	Asn	Glu	
65				70					75						80	
Pro	Val	Ile	Ile	Lys	Arg	Leu	Leu	Asp	Ile	Gly	Phe	Tyr	Asn	Phe	Leu	
			85					90					95			
Ile	Pro	Phe	Val	Glu	Thr	Lys	Glu	Glu	Ala	Glu	Leu	Ala	Val	Ala	Ser	
		100						105					110			
Thr	Arg	Tyr	Pro	Pro	Glu	Gly	Ile	Arg	Gly	Val	Ser	Val	Ser	His	Arg	
	115					120						125				
Ala	Asn	Met	Phe	Gly	Thr	Val	Ala	Asp	Tyr	Phe	Ala	Gln	Ser	Asn	Lys	
	130					135					140					
Asn	Ile	Thr	Ile	Leu	Val	Gln	Ile	Glu	Ser	Gln	Gln	Gly	Val	Asp	Asn	
145				150					155					160		
Val	Asp	Ala	Ile	Ala	Ala	Thr	Glu	Gly	Val	Asp	Gly	Ile	Phe	Val	Gly	
			165					170						175		

Pro Ser Asp Leu Ala Ala Ala Leu Gly His Leu Gly Asn Ala Ser His
180 185 190
Pro Asp Val Gln Lys Ala Ile Gln His Ile Phe Asn Arg Ala Ser Ala
195 200 205
His Gly Lys Pro Ser Gly Ile Leu Ala Pro Val Glu Ala Asp Ala Arg
210 215 220
Arg Tyr Leu Glu Trp Gly Ala Thr Phe Val Ala Val Gly Ser Asp Leu
225 230 235 240
Gly Val Phe Arg Ser Ala Thr Gln Lys Leu Ala Asp Thr Phe Lys Lys
245 250 255

<210> 258
<211> 444
<212> PRT
<213> E. Coli

<400> 258

Met Ile Leu Asp Thr Val Asp Glu Lys Lys Lys Gly Val His Thr Arg
1 5 10 15
Tyr Leu Ile Leu Leu Ile Ile Phe Ile Val Thr Ala Val Asn Tyr Ala
20 25 30
Asp Arg Ala Thr Leu Ser Ile Ala Gly Thr Glu Val Ala Lys Glu Leu
35 40 45
Gln Leu Ser Ala Val Ser Met Gly Tyr Ile Phe Ser Ala Phe Gly Trp
50 55 60
Ala Tyr Leu Leu Met Gln Ile Pro Gly Gly Trp Leu Leu Asp Lys Phe
65 70 75 80
Gly Ser Lys Lys Val Tyr Thr Tyr Ser Leu Phe Phe Trp Ser Leu Phe
85 90 95
Thr Phe Leu Gln Gly Phe Val Asp Met Phe Pro Leu Ala Trp Ala Gly
100 105 110
Ile Ser Met Phe Phe Met Arg Phe Met Leu Gly Phe Ser Glu Ala Pro
115 120 125
Ser Phe Pro Ala Asn Ala Arg Ile Val Ala Ala Trp Phe Pro Thr Lys
130 135 140
Glu Arg Gly Thr Ala Ser Ala Ile Phe Asn Ser Ala Gln Tyr Phe Ser
145 150 155 160
Leu Ala Leu Phe Ser Pro Leu Leu Gly Trp Leu Thr Phe Ala Trp Gly
165 170 175
Trp Glu His Val Phe Thr Val Met Gly Val Ile Gly Phe Val Leu Thr
180 185 190
Ala Leu Trp Ile Lys Leu Ile His Asn Pro Thr Asp His Pro Arg Met
195 200 205
Ser Ala Glu Glu Leu Lys Phe Ile Ser Glu Asn Gly Ala Val Val Asp
210 215 220
Met Asp His Lys Lys Pro Gly Ser Ala Ala Ser Gly Pro Lys Leu
225 230 235 240
His Tyr Ile Lys Gln Leu Leu Ser Asn Arg Met Met Leu Gly Val Phe
245 250 255
Phe Gly Gln Tyr Phe Ile Asn Thr Ile Thr Trp Phe Phe Leu Thr Trp
260 265 270
Phe Pro Ile Tyr Leu Val Gln Glu Lys Gly Met Ser Ile Leu Lys Val
275 280 285
Gly Leu Val Ala Ser Ile Pro Ala Leu Cys Gly Phe Ala Gly Gly Val
290 295 300
Leu Gly Gly Val Phe Ser Asp Tyr Leu Ile Lys Arg Gly Leu Ser Leu

305 310 315 320
 Thr Leu Ala Arg Lys Leu Pro Ile Val Leu Gly Met Leu Leu Ala Ser
 325 330 335
 Thr Ile Ile Leu Cys Asn Tyr Thr Asn Asn Thr Thr Leu Val Val Met
 340 345 350
 Leu Met Ala Leu Ala Phe Phe Gly Lys Gly Phe Gly Ala Leu Gly Trp
 355 360 365
 Pro Val Ile Ser Asp Thr Ala Pro Lys Glu Ile Val Gly Leu Cys Gly
 370 375 380
 Gly Val Phe Asn Val Phe Gly Asn Val Ala Ser Ile Val Thr Pro Leu
 385 390 395 400
 Val Ile Gly Tyr Leu Val Ser Glu Leu His Ser Phe Asn Ala Ala Leu
 405 410 415
 Val Phe Val Gly Cys Ser Ala Leu Met Ala Met Val Cys Tyr Leu Phe
 420 425 430
 Val Val Gly Asp Ile Lys Arg Met Glu Leu Gln Lys
 435 440

<210> 259
 <211> 511
 <212> PRT
 <213> E. Coli

<400> 259
 Met Gln Thr Ser Asp Thr Arg Ala Leu Pro Leu Leu Cys Ala Arg Ser
 1 5 10 15
 Val Tyr Lys Gln Tyr Ser Gly Val Asn Val Leu Lys Gly Ile Asp Phe
 20 25 30
 Thr Leu His Gln Gly Glu Val His Ala Leu Leu Gly Gly Asn Gly Ala
 35 40 45
 Gly Lys Ser Thr Leu Met Lys Ile Ile Ala Gly Ile Thr Pro Ala Asp
 50 55 60
 Ser Gly Thr Leu Glu Ile Glu Gly Asn Asn Tyr Val Arg Leu Thr Pro
 65 70 75 80
 Val His Ala His Gln Leu Gly Ile Tyr Leu Val Pro Gln Glu Pro Leu
 85 90 95
 Leu Phe Pro Ser Leu Ser Ile Lys Glu Asn Ile Leu Phe Gly Leu Ala
 100 105 110
 Lys Lys Gln Leu Ser Met Gln Lys Met Lys Asn Leu Leu Ala Ala Leu
 115 120 125
 Gly Cys Gln Phe Asp Leu His Ser Leu Ala Gly Ser Leu Asp Val Ala
 130 135 140
 Asp Arg Gln Met Val Glu Ile Leu Arg Gly Leu Met Arg Asp Ser Arg
 145 150 155 160
 Ile Leu Ile Leu Asp Glu Pro Thr Ala Ser Leu Thr Pro Ala Glu Thr
 165 170 175
 Glu Arg Leu Phe Ser Arg Leu Gln Glu Leu Leu Ala Thr Gly Val Gly
 180 185 190
 Ile Val Phe Ile Ser His Lys Leu Pro Glu Ile Arg Gln Ile Ala Asp
 195 200 205
 Arg Ile Ser Val Met Arg Asp Gly Thr Ile Ala Leu Ser Gly Lys Thr
 210 215 220
 Ser Glu Leu Ser Thr Asp Asp Ile Ile Gln Ala Ile Thr Pro Ala Val
 225 230 235 240
 Arg Glu Lys Ser Leu Ser Ala Ser Gln Lys Leu Trp Leu Glu Leu Pro
 245 250 255

Gly Asn Arg Pro Gln His Ala Ala Gly Thr Pro Val Leu Thr Leu Glu
 260 265 270
 Asn Leu Thr Gly Glu Gly Phe Arg Asn Val Ser Leu Thr Leu Asn Ala
 275 280 285
 Gly Glu Ile Leu Gly Leu Ala Gly Leu Val Gly Ala Gly Arg Thr Glu
 290 295 300
 Leu Ala Glu Thr Leu Tyr Gly Leu Arg Thr Leu Arg Gly Gly Arg Ile
 305 310 315 320
 Met Leu Asn Gly Lys Glu Ile Asn Lys Leu Ser Thr Gly Glu Arg Leu
 325 330 335
 Leu Arg Gly Leu Val Tyr Leu Pro Glu Asp Arg Gln Ser Ser Gly Leu
 340 345 350
 Asn Leu Asp Ala Ser Leu Ala Trp Asn Val Cys Ala Leu Thr His Asn
 355 360 365
 Leu Arg Gly Phe Trp Ala Lys Thr Ala Lys Asp Asn Ala Thr Leu Glu
 370 375 380
 Arg Tyr Arg Arg Ala Leu Asn Ile Lys Phe Asn Gln Pro Glu Gln Ala
 385 390 395 400
 Ala Arg Thr Leu Ser Gly Gly Asn Gln Gln Lys Ile Leu Ile Ala Lys
 405 410 415
 Cys Leu Glu Ala Ser Pro Gln Val Leu Ile Val Asp Glu Pro Thr Arg
 420 425 430
 Gly Val Asp Val Ser Ala Arg Asn Asp Ile Tyr Gln Leu Leu Arg Ser
 435 440 445
 Ile Ala Ala Gln Asn Val Ala Val Leu Leu Ile Ser Ser Asp Leu Glu
 450 455 460
 Glu Ile Glu Leu Met Ala Asp Arg Val Tyr Val Met His Gln Gly Glu
 465 470 475 480
 Ile Thr His Ser Ala Leu Thr Glu Arg Asp Ile Asn Val Glu Thr Ile
 485 490 495
 Met Arg Val Ala Phe Gly Asp Ser Gln Arg Gln Glu Ala Ser Cys
 500 505 510

<210> 260
 <211> 342
 <212> PRT
 <213> E. Coli

<400> 260
 Met Leu Lys Phe Ile Gln Asn Asn Arg Glu Ile Thr Ala Leu Leu Ala
 1 5 10 15
 Val Val Leu Leu Phe Val Leu Pro Gly Phe Leu Asp Arg Gln Tyr Leu
 20 25 30
 Ser Val Gln Thr Leu Thr Met Val Tyr Ser Ser Ala Gln Ile Leu Ile
 35 40 45
 Leu Leu Ala Met Gly Ala Thr Leu Val Met Leu Thr Arg Asn Ile Asp
 50 55 60
 Val Ser Val Gly Ser Ile Thr Gly Met Cys Ala Val Leu Leu Gly Met
 65 70 75 80
 Leu Leu Asn Ala Gly Tyr Ser Leu Pro Val Ala Cys Val Ala Thr Leu
 85 90 95
 Leu Leu Gly Leu Leu Ala Gly Phe Phe Asn Gly Val Leu Val Ala Trp
 100 105 110
 Leu Lys Ile Pro Ala Ile Val Ala Thr Leu Gly Thr Leu Gly Leu Tyr
 115 120 125
 Arg Gly Ile Met Leu Leu Trp Thr Gly Gly Lys Trp Ile Glu Gly Leu

Leu Pro Ala Ala Ala Gln Ala Ala Glu Asn Leu Lys Asn Asp Lys Val
 225 230 235 240
 Ala Ile Val Gly Phe Ser Thr Pro Asn Val Met Arg Pro Tyr Val Glu
 245 250 255
 Arg Gly Thr Val Lys Glu Phe Gly Leu Trp Asp Val Val Gln Gln Gly
 260 265 270
 Lys Ile Ser Val Tyr Val Ala Asp Ala Leu Leu Lys Lys Gly Ser Met
 275 280 285
 Lys Thr Gly Asp Lys Leu Asp Ile Lys Gly Val Gly Gln Val Glu Val
 290 295 300
 Ser Pro Asn Ser Val Gln Gly Tyr Asp Tyr Glu Ala Asp Gly Asn Gly
 305 310 315 320
 Ile Val Leu Leu Pro Glu Arg Val Ile Phe Asn Lys Glu Asn Ile Gly
 325 330 335
 Lys Tyr Asp Phe
 340

<210> 263
 <211> 291
 <212> PRT
 <213> E. Coli

<400> 263

Met Ala Asp Leu Asp Asp Ile Lys Asp Gly Lys Asp Phe Arg Thr Asp
 1 5 10 15
 Gln Pro Gln Lys Asn Ile Pro Phe Thr Leu Lys Gly Cys Gly Ala Leu
 20 25 30
 Asp Trp Gly Met Gln Ser Arg Leu Ser Arg Ile Phe Asn Pro Lys Thr
 35 40 45
 Gly Lys Thr Val Met Leu Ala Phe Asp His Gly Tyr Phe Gln Gly Pro
 50 55 60
 Thr Thr Gly Leu Glu Arg Ile Asp Ile Asn Ile Ala Pro Leu Phe Glu
 65 70 75 80
 His Ala Asp Val Leu Met Cys Thr Arg Gly Ile Leu Arg Ser Val Val
 85 90 95
 Pro Pro Ala Thr Asn Arg Pro Val Val Leu Arg Ala Ser Gly Ala Asn
 100 105 110
 Ser Ile Leu Ala Glu Leu Ser Asn Glu Ala Val Ala Leu Ser Met Asp
 115 120 125
 Asp Ala Val Arg Leu Asn Ser Cys Ala Val Ala Ala Gln Val Tyr Ile
 130 135 140
 Gly Ser Glu Tyr Glu His Gln Ser Ile Lys Asn Ile Ile Gln Leu Val
 145 150 155 160
 Asp Ala Gly Met Lys Val Gly Met Pro Thr Met Ala Val Thr Gly Val
 165 170 175
 Gly Lys Asp Met Val Arg Asp Gln Arg Tyr Phe Ser Leu Ala Thr Arg
 180 185 190
 Ile Ala Ala Glu Met Gly Ala Gln Ile Ile Lys Thr Tyr Tyr Val Glu
 195 200 205
 Lys Gly Phe Glu Arg Ile Val Ala Gly Cys Pro Val Pro Ile Val Ile
 210 215 220
 Ala Gly Gly Lys Lys Leu Pro Glu Arg Glu Ala Leu Glu Met Cys Trp
 225 230 235 240
 Gln Ala Ile Asp Gln Gly Ala Ser Gly Val Asp Met Gly Arg Asn Ile
 245 250 255
 Phe Gln Ser Asp His Pro Val Ala Met Met Lys Ala Val Gln Ala Val

	260		265		270										
Val	His	His	Asn	Glu	Thr	Ala	Asp	Arg	Ala	Tyr	Glu	Leu	Tyr	Leu	Ser
	275		280									285			
Glu	Lys	Gln													
	290														

<210> 264
 <211> 96
 <212> PRT
 <213> E. Coli

<400> 264															
Met	His	Val	Thr	Leu	Val	Glu	Ile	Asn	Val	His	Glu	Asp	Lys	Val	Asp
1				5					10					15	
Glu	Phe	Ile	Glu	Val	Phe	Arg	Gln	Asn	His	Leu	Gly	Ser	Val	Gln	Glu
			20					25					30		
Glu	Gly	Asn	Leu	Arg	Phe	Asp	Val	Leu	Gln	Asp	Pro	Glu	Val	Asn	Ser
		35					40					45			
Arg	Phe	Tyr	Ile	Tyr	Glu	Ala	Tyr	Lys	Asp	Glu	Asp	Ala	Val	Ala	Phe
	50					55				60					
His	Lys	Thr	Thr	Pro	His	Tyr	Lys	Thr	Cys	Val	Ala	Lys	Leu	Glu	Ser
65				70					75					80	
Leu	Met	Thr	Gly	Pro	Arg	Lys	Lys	Arg	Leu	Phe	Asn	Gly	Leu	Met	Pro
				85				90					95		

<210> 265
 <211> 383
 <212> PRT
 <213> E. Coli

<400> 265															
Met	Phe	Glu	Pro	Met	Glu	Leu	Thr	Asn	Asp	Ala	Val	Ile	Lys	Val	Ile
1				5					10					15	
Gly	Val	Gly	Gly	Gly	Gly	Gly	Gly	Asn	Ala	Val	Glu	His	Met	Val	Arg
			20					25						30	
Arg	Ile	Glu	Gly	Val	Glu	Phe	Phe	Ala	Val	Asn	Thr	Asp	Ala	Gln	Ala
			35				40					45			
Leu	Arg	Lys	Thr	Ala	Val	Gly	Gln	Thr	Ile	Gln	Ile	Gly	Ser	Gly	Ile
	50					55				60					
Thr	Lys	Gly	Leu	Gly	Ala	Gly	Ala	Asn	Pro	Glu	Val	Gly	Arg	Asn	Ala
65				70				75						80	
Ala	Asp	Glu	Asp	Arg	Asp	Ala	Leu	Arg	Ala	Ala	Leu	Glu	Gly	Ala	Asp
			85					90					95		
Met	Val	Phe	Ile	Ala	Ala	Gly	Met	Gly	Gly	Gly	Thr	Gly	Thr	Gly	Ala
			100				105						110		
Ala	Pro	Val	Val	Ala	Glu	Val	Ala	Lys	Asp	Leu	Gly	Ile	Leu	Thr	Val
		115					120					125			
Ala	Val	Val	Thr	Lys	Pro	Phe	Asn	Phe	Glu	Gly	Lys	Lys	Arg	Met	Ala
	130					135					140				
Phe	Ala	Glu	Gln	Gly	Ile	Thr	Glu	Leu	Ser	Lys	His	Val	Asp	Ser	Leu
145				150					155					160	
Ile	Thr	Ile	Pro	Asn	Asp	Lys	Leu	Leu	Lys	Val	Leu	Gly	Arg	Gly	Ile
			165					170					175		
Ser	Leu	Leu	Asp	Ala	Phe	Gly	Ala	Ala	Asn	Asp	Val	Leu	Lys	Gly	Ala
			180				185					190			

Val	Gln	Gly	Ile	Ala	Glu	Leu	Ile	Thr	Arg	Pro	Gly	Leu	Met	Asn	Val
	195						200					205			
Asp	Phe	Ala	Asp	Val	Arg	Thr	Val	Met	Ser	Glu	Met	Gly	Tyr	Ala	Met
	210						215				220				
Met	Gly	Ser	Gly	Val	Ala	Ser	Gly	Glu	Asp	Arg	Ala	Glu	Glu	Ala	Ala
225					230					235					240
Glu	Met	Ala	Ile	Ser	Ser	Pro	Leu	Leu	Glu	Asp	Ile	Asp	Leu	Ser	Gly
			245						250					255	
Ala	Arg	Gly	Val	Leu	Val	Asn	Ile	Thr	Ala	Gly	Phe	Asp	Leu	Arg	Leu
			260					265					270		
Asp	Glu	Phe	Glu	Thr	Val	Gly	Asn	Thr	Ile	Arg	Ala	Phe	Ala	Ser	Asp
	275						280					285			
Asn	Ala	Thr	Val	Val	Ile	Gly	Thr	Ser	Leu	Asp	Pro	Asp	Met	Asn	Asp
	290					295					300				
Glu	Leu	Arg	Val	Thr	Val	Val	Ala	Thr	Gly	Ile	Gly	Met	Asp	Lys	Arg
305					310					315					320
Pro	Glu	Ile	Thr	Leu	Val	Thr	Asn	Lys	Gln	Val	Gln	Gln	Pro	Val	Met
			325						330					335	
Asp	Arg	Tyr	Gln	Gln	His	Gly	Met	Ala	Pro	Leu	Thr	Gln	Glu	Gln	Lys
			340					345					350		
Pro	Val	Ala	Lys	Val	Val	Asn	Asp	Asn	Ala	Pro	Gln	Thr	Ala	Lys	Glu
	355					360						365			
Pro	Asp	Tyr	Leu	Asp	Ile	Pro	Ala	Phe	Leu	Arg	Lys	Gln	Ala	Asp	
	370					375						380			

<210> 266
 <211> 1014
 <212> PRT
 <213> E. Coli

<400> 266

Met	Asp	Val	Ser	Arg	Arg	Gln	Phe	Phe	Lys	Ile	Cys	Ala	Gly	Gly	Met
1				5					10					15	
Ala	Gly	Thr	Thr	Val	Ala	Ala	Leu	Gly	Phe	Ala	Pro	Lys	Gln	Ala	Leu
			20					25					30		
Ala	Gln	Ala	Arg	Asn	Tyr	Lys	Leu	Leu	Arg	Ala	Lys	Glu	Ile	Arg	Asn
		35				40						45			
Thr	Cys	Thr	Tyr	Cys	Ser	Val	Gly	Cys	Gly	Leu	Leu	Met	Tyr	Ser	Leu
	50			55						60					
Gly	Asp	Gly	Ala	Lys	Asn	Ala	Arg	Glu	Ala	Ile	Tyr	His	Ile	Glu	Gly
65				70					75				80		
Asp	Pro	Asp	His	Pro	Val	Ser	Arg	Gly	Ala	Leu	Cys	Pro	Lys	Gly	Ala
			85					90					95		
Gly	Leu	Leu	Asp	Tyr	Val	Asn	Ser	Glu	Asn	Arg	Leu	Arg	Tyr	Pro	Glu
		100						105					110		
Tyr	Arg	Ala	Pro	Gly	Ser	Asp	Lys	Trp	Gln	Arg	Ile	Ser	Trp	Glu	Glu
		115				120						125			
Ala	Phe	Ser	Arg	Ile	Ala	Lys	Leu	Met	Lys	Ala	Asp	Arg	Asp	Ala	Asn
	130				135					140					
Phe	Ile	Glu	Lys	Asn	Glu	Gln	Gly	Val	Thr	Val	Asn	Arg	Trp	Leu	Ser
145				150					155					160	
Thr	Gly	Met	Leu	Cys	Ala	Ser	Gly	Ala	Ser	Asn	Glu	Thr	Gly	Met	Leu
			165				170						175		
Thr	Gln	Lys	Phe	Ala	Arg	Ser	Leu	Gly	Met	Leu	Ala	Val	Asp	Asn	Gln
		180					185					190			
Ala	Arg	Val	His	Gly	Pro	Thr	Val	Ala	Ser	Leu	Ala	Pro	Thr	Phe	Gly

His His Leu Arg Glu Leu Tyr Gln Ser Glu Gly Gly Lys Gly Val Glu
 660 665 670
 Pro Leu Met Lys Met Ser Trp Asn Tyr Lys Gln Pro His Glu Pro Gln
 675 680 685
 Ser Asp Glu Val Ala Lys Glu Asn Asn Gly Tyr Ala Leu Glu Asp Leu
 690 695 700
 Tyr Asp Ala Asn Gly Val Leu Ile Ala Lys Lys Gly Gln Leu Leu Ser
 705 710 715 720
 Ser Phe Ala His Leu Arg Asp Asp Gly Thr Thr Ala Ser Ser Cys Trp
 725 730 735
 Ile Tyr Thr Gly Ser Trp Thr Glu Gln Gly Asn Gln Met Ala Asn Arg
 740 745 750
 Asp Asn Ser Asp Pro Ser Gly Leu Gly Asn Thr Leu Gly Trp Ala Trp
 755 760 765
 Ala Trp Pro Leu Asn Arg Arg Val Leu Tyr Asn Arg Ala Ser Ala Asp
 770 775 780
 Ile Asn Gly Lys Pro Trp Asp Pro Lys Arg Met Leu Ile Gln Trp Asn
 785 790 795 800
 Gly Ser Lys Trp Thr Gly Asn Asp Ile Pro Asp Phe Gly Asn Ala Ala
 805 810 815
 Pro Gly Thr Pro Thr Gly Pro Phe Ile Met Gln Pro Glu Gly Met Gly
 820 825 830
 Arg Leu Phe Ala Ile Asn Lys Met Ala Glu Gly Pro Phe Pro Glu His
 835 840 845
 Tyr Glu Pro Ile Glu Thr Pro Leu Gly Thr Asn Pro Leu His Pro Asn
 850 855 860
 Val Val Ser Asn Pro Val Arg Leu Tyr Glu Gln Asp Ala Leu Arg
 865 870 875 880
 Met Gly Lys Lys Glu Gln Phe Pro Tyr Val Gly Thr Thr Tyr Arg Leu
 885 890 895
 Thr Glu His Phe His Thr Trp Thr Lys His Ala Leu Leu Asn Ala Ile
 900 905 910
 Ala Gln Pro Glu Gln Phe Val Glu Ile Ser Glu Thr Leu Ala Ala Ala
 915 920 925
 Lys Gly Ile Asn Asn Gly Asp Arg Val Thr Val Ser Ser Lys Arg Gly
 930 935 940
 Phe Ile Arg Ala Val Ala Val Val Thr Arg Arg Leu Lys Pro Leu Asn
 945 950 955 960
 Val Asn Gly Gln Gln Val Glu Thr Val Gly Ile Pro Ile His Trp Gly
 965 970 975
 Phe Glu Gly Val Ala Arg Lys Gly Tyr Ile Ala Asn Thr Leu Thr Pro
 980 985 990
 Asn Val Gly Asp Ala Asn Ser Gln Thr Pro Glu Tyr Lys Ala Phe Leu
 995 1000 1005
 Val Asn Ile Glu Lys Ala
 1010

<210> 267
 <211> 294
 <212> PRT
 <213> E. Coli

<400> 267

Met Ala Met Glu Thr Gln Asp Ile Ile Lys Arg Ser Ala Thr Asn Ser
 1 5 10 15
 Ile Thr Pro Pro Ser Gln Val Arg Asp Tyr Lys Ala Glu Val Ala Lys
 20 25 30

Leu Ile Asp Val Ser Thr Cys Ile Gly Cys Lys Ala Cys Gln Val Ala
 35 40 45
 Cys Ser Glu Trp Asn Asp Ile Arg Asp Glu Val Gly His Cys Val Gly
 50 55 60
 Val Tyr Asp Asn Pro Ala Asp Leu Ser Ala Lys Ser Trp Thr Val Met
 65 70 75 80
 Arg Phe Ser Glu Thr Glu Gln Asn Gly Lys Leu Glu Trp Leu Ile Arg
 85 90 95
 Lys Asp Gly Cys Met His Cys Glu Asp Pro Gly Cys Leu Lys Ala Cys
 100 105 110
 Pro Ser Ala Gly Ala Ile Ile Gln Tyr Ala Asn Gly Ile Val Asp Phe
 115 120 125
 Gln Ser Glu Asn Cys Ile Gly Cys Gly Tyr Cys Ile Ala Gly Cys Pro
 130 135 140
 Phe Asn Ile Pro Arg Leu Asn Lys Glu Asp Asn Arg Val Tyr Lys Cys
 145 150 155 160
 Thr Leu Cys Val Asp Arg Val Ser Val Gly Gln Glu Pro Ala Cys Val
 165 170 175
 Lys Thr Cys Pro Thr Gly Ala Ile His Phe Gly Thr Lys Lys Glu Met
 180 185 190
 Leu Glu Leu Ala Glu Gln Arg Val Ala Lys Leu Lys Ala Arg Gly Tyr
 195 200 205
 Glu His Ala Gly Val Tyr Asn Pro Glu Gly Val Gly Gly Thr His Val
 210 215 220
 Met Tyr Val Leu His His Ala Asp Gln Pro Glu Leu Tyr His Gly Leu
 225 230 235 240
 Pro Lys Asp Pro Lys Ile Asp Thr Ser Val Ser Leu Trp Lys Gly Ala
 245 250 255
 Leu Lys Pro Leu Ala Ala Ala Gly Phe Ile Ala Thr Phe Ala Gly Leu
 260 265 270
 Ile Phe His Tyr Ile Gly Ile Gly Pro Asn Lys Glu Val Asp Asp Asp
 275 280 285
 Glu Glu Asp His His Glu
 290

<210> 268
 <211> 217
 <212> PRT
 <213> E. Coli

<400> 268
 Met Ser Lys Ser Lys Met Ile Val Arg Thr Lys Phe Ile Asp Arg Ala
 1 5 10 15
 Cys His Trp Thr Val Val Ile Cys Phe Phe Leu Val Ala Leu Ser Gly
 20 25 30
 Ile Ser Phe Phe Pro Thr Leu Gln Trp Leu Thr Gln Thr Phe Gly
 35 40 45
 Thr Pro Gln Met Gly Arg Ile Leu His Pro Phe Phe Gly Ile Ala Ile
 50 55 60
 Phe Val Ala Leu Met Phe Met Phe Val Arg Phe Val His His Asn Ile
 65 70 75 80
 Pro Asp Lys Lys Asp Ile Pro Trp Leu Leu Asn Ile Val Glu Val Leu
 85 90 95
 Lys Gly Asn Glu His Lys Val Ala Asp Val Gly Lys Tyr Asn Ala Gly
 100 105 110
 Gln Lys Met Met Phe Trp Ser Ile Met Ser Met Ile Phe Val Leu Leu

115	120	125
Val Thr Gly Val Ile Ile Trp Arg Pro Tyr Phe Ala Gln Tyr Phe Pro		
130	135	140
Met Gln Val Val Arg Tyr Ser Leu Leu Ile His Ala Ala Ala Gly Ile		
145	150	155
Ile Leu Ile His Ala Ile Leu Ile His Met Tyr Met Ala Phe Trp Val		
165	170	175
Lys Gly Ser Ile Lys Gly Met Ile Glu Gly Lys Val Ser Arg Arg Trp		
180	185	190
Ala Lys Lys His His Pro Arg Trp Tyr Arg Glu Ile Glu Lys Ala Glu		
195	200	205
Ala Lys Lys Glu Ser Glu Glu Gly Ile		
210	215	

<210> 269
 <211> 86
 <212> PRT
 <213> E. Coli

<400> 269
Met Ala Leu Leu Ile Thr Lys Lys Cys Ile Asn Cys Asp Met Cys Glu
1 5 10 15
Pro Glu Cys Pro Asn Glu Ala Ile Ser Met Gly Asp His Ile Tyr Glu
20 25 30
Ile Asn Ser Asp Lys Cys Thr Glu Cys Val Gly His Tyr Glu Thr Pro
35 40 45
Thr Cys Gln Lys Val Cys Pro Ile Pro Asn Thr Ile Val Lys Asp Pro
50 55 60
Ala His Val Glu Thr Glu Glu Gln Leu Trp Asp Lys Phe Val Leu Met
65 70 75 80
His His Ala Asp Lys Ile
85

<210> 270
 <211> 400
 <212> PRT
 <213> E. Coli

<400> 270
Met Gln Ser Val Asp Val Ala Ile Val Gly Gly Gly Met Val Gly Leu
1 5 10 15
Ala Val Ala Cys Gly Leu Gln Gly Ser Gly Leu Arg Val Ala Val Leu
20 25 30
Glu Gln Arg Val Gln Glu Pro Leu Ala Ala Asn Ala Pro Pro Gln Leu
35 40 45
Arg Val Ser Ala Ile Asn Ala Ala Ser Glu Lys Leu Leu Thr Arg Leu
50 55 60
Gly Val Trp Gln Asp Ile Leu Ser Arg Arg Ala Ser Cys Tyr His Gly
65 70 75 80
Met Glu Val Trp Asp Lys Asp Ser Phe Gly His Ile Ser Phe Asp Asp
85 90 95
Gln Ser Met Gly Tyr Ser His Leu Gly His Ile Val Glu Asn Ser Val
100 105 110
Ile His Tyr Ala Leu Trp Asn Lys Ala His Gln Ser Ser Asp Ile Thr
115 120 125

Leu	Leu	Ala	Pro	Ala	Glu	Leu	Gln	Gln	Val	Ala	Trp	Gly	Glu	Asn	Glu
130						135					140				
Thr	Phe	Leu	Thr	Leu	Lys	Asp	Gly	Ser	Met	Leu	Thr	Ala	Arg	Leu	Val
145					150					155					160
Ile	Gly	Ala	Asp	Gly	Ala	Asn	Ser	Trp	Leu	Arg	Asn	Lys	Ala	Asp	Ile
			165						170					175	
Pro	Leu	Thr	Phe	Trp	Asp	Tyr	Gln	His	His	Ala	Leu	Val	Ala	Thr	Ile
			180					185						190	
Arg	Thr	Glu	Glu	Pro	His	Asp	Ala	Val	Ala	Arg	Gln	Val	Phe	His	Gly
		195					200					205			
Glu	Gly	Ile	Leu	Ala	Phe	Leu	Pro	Leu	Ser	Asp	Pro	His	Leu	Cys	Ser
	210					215					220				
Ile	Val	Trp	Ser	Leu	Ser	Pro	Glu	Glu	Ala	Gln	Arg	Met	Gln	Gln	Ala
225					230					235					240
Ser	Glu	Asp	Glu	Phe	Asn	Arg	Ala	Leu	Asn	Ile	Ala	Phe	Asp	Asn	Arg
				245					250					255	
Leu	Gly	Leu	Cys	Lys	Val	Glu	Ser	Ala	Arg	Gln	Val	Phe	Pro	Leu	Thr
			260					265						270	
Gly	Arg	Tyr	Ala	Arg	Gln	Phe	Ala	Ser	His	Arg	Leu	Ala	Leu	Val	Gly
		275					280					285			
Asp	Ala	Ala	His	Thr	Ile	His	Pro	Leu	Ala	Gly	Gln	Gly	Val	Asn	Leu
		290				295					300				
Gly	Phe	Met	Asp	Ala	Ala	Glu	Leu	Ile	Ala	Glu	Leu	Lys	Arg	Leu	His
305					310					315					320
Arg	Gln	Gly	Lys	Asp	Ile	Gly	Gln	Tyr	Ile	Tyr	Leu	Arg	Arg	Tyr	Glu
				325					330					335	
Arg	Ser	Arg	Lys	His	Ser	Ala	Ala	Leu	Met	Leu	Ala	Gly	Met	Gln	Gly
			340					345						350	
Phe	Arg	Asp	Leu	Phe	Ser	Gly	Thr	Asn	Pro	Ala	Lys	Lys	Leu	Leu	Arg
		355					360					365			
Asp	Ile	Gly	Leu	Lys	Leu	Ala	Asp	Thr	Leu	Pro	Gly	Val	Lys	Pro	Gln
	370					375					380				
Leu	Ile	Arg	Gln	Ala	Met	Gly	Leu	Asn	Asp	Leu	Pro	Glu	Trp	Leu	Arg
385					390					395					400

<210> 271
 <211> 392
 <212> PRT
 <213> E. Coli

<400> 271															
Met	Ser	Val	Ile	Ile	Val	Gly	Gly	Gly	Met	Ala	Gly	Ala	Thr	Leu	Ala
1				5					10					15	
Leu	Ala	Ile	Ser	Arg	Leu	Ser	His	Gly	Ala	Leu	Pro	Val	His	Leu	Ile
			20					25					30		
Glu	Ala	Thr	Ala	Pro	Glu	Ser	His	Ala	His	Pro	Gly	Phe	Asp	Gly	Arg
		35					40					45			
Ala	Ile	Ala	Leu	Ala	Ala	Gly	Thr	Cys	Gln	Gln	Leu	Ala	Arg	Ile	Gly
	50					55					60				
Val	Trp	Gln	Ser	Leu	Ala	Asp	Cys	Ala	Thr	Ala	Ile	Thr	Thr	Val	His
65					70					75					80
Val	Ser	Asp	Arg	Gly	His	Ala	Gly	Phe	Val	Thr	Leu	Ala	Ala	Glu	Asp
				85					90					95	
Tyr	Gln	Leu	Ala	Ala	Leu	Gly	Gln	Val	Val	Glu	Leu	His	Asn	Val	Gly
			100					105					110		
Gln	Arg	Leu	Phe	Ala	Leu	Leu	Arg	Lys	Ala	Pro	Gly	Val	Thr	Leu	His

Glu Ile Asn Gln Gln Leu Tyr Gln Leu Leu Asn Gly Leu Asp Val Val
 115 120 125
 Tyr His Ala Gln Gly Glu Tyr Ala Tyr Ala Asp Val Ile Val Asn Ser
 130 135 140
 Ala Leu Glu Lys Leu Arg Lys Gly Ser Arg Gln Asn Leu Thr Ala Pro
 145 150 155 160
 Ala Thr Met Ile Asp Trp Arg Pro Val Val His Glu Met Arg Leu Phe
 165 170 175
 Lys Ser Pro Glu Glu Ile Ala Val Leu Arg Arg Ala Gly Glu Ile Thr
 180 185 190
 Ala Met Ala His Thr Arg Ala Met Glu Lys Cys Arg Pro Gly Met Phe
 195 200 205
 Glu Tyr His Leu Glu Gly Glu Ile His His Glu Phe Asn Arg His Gly
 210 215 220
 Ala Arg Tyr Pro Ser Tyr Asn Thr Ile Val Gly Ser Gly Glu Asn Gly
 225 230 235 240
 Cys Ile Leu His Tyr Thr Glu Asn Glu Cys Glu Met Arg Asp Gly Asp
 245 250 255
 Leu Val Leu Ile Asp Ala Gly Cys Glu Tyr Lys Gly Tyr Ala Gly Asp
 260 265 270
 Ile Thr Arg Thr Phe Pro Val Asn Gly Lys Phe Thr Gln Ala Gln Arg
 275 280 285
 Glu Ile Tyr Asp Ile Val Leu Glu Ser Leu Glu Thr Ser Leu Arg Leu
 290 295 300
 Tyr Arg Pro Gly Thr Ser Ile Leu Glu Val Thr Gly Glu Val Val Arg
 305 310 315 320
 Ile Met Val Ser Gly Leu Val Lys Leu Gly Ile Leu Lys Gly Asp Val
 325 330 335
 Asp Glu Leu Ile Ala Gln Asn Ala His Arg Pro Phe Phe Met His Gly
 340 345 350
 Leu Ser His Trp Leu Gly Leu Asp Val His Asp Val Gly Val Tyr Gly
 355 360 365
 Gln Asp Arg Ser Arg Ile Leu Glu Pro Gly Met Val Leu Thr Val Glu
 370 375 380
 Pro Gly Leu Tyr Ile Ala Pro Asp Ala Glu Val Pro Glu Gln Tyr Arg
 385 390 395 400
 Gly Ile Gly Ile Arg Ile Glu Asp Asp Ile Val Ile Thr Glu Thr Gly
 405 410 415
 Asn Glu Asn Leu Thr Ala Ser Val Val Lys Lys Pro Glu Glu Ile Glu
 420 425 430
 Ala Leu Met Val Ala Ala Arg Lys Gln
 435 440

<210> 273

<211> 194

<212> PRT

<213> E. Coli

<400> 273

Met Leu Met Ser Ile Gln Asn Glu Met Pro Gly Tyr Asn Glu Met Asn
 1 5 10 15
 Gln Tyr Leu Asn Gln Gln Gly Thr Gly Leu Thr Pro Ala Glu Met His
 20 25 30
 Gly Leu Ile Ser Gly Met Ile Cys Gly Gly Asn Asp Asp Ser Ser Trp
 35 40 45
 Leu Pro Leu Leu His Asp Leu Thr Asn Glu Gly Met Ala Phe Gly His

50		55		60	
Glu	Leu	Ala	Gln	Ala	Leu
65		70		75	
Leu	Gln	Asp	Asp	Gly	Phe
		85		90	
Asp	Val	Ser	Val	Phe	Asp
		100		105	
His	Phe	Leu	Gly	Leu	Gly
		115		120	
Thr	Gly	Glu	Thr	Gly	Glu
		130		135	
Leu	Gly	Tyr	Asp	Glu	Asp
		145		150	
Glu	Glu	Ile	Ile	Glu	Tyr
		165		170	
Thr	Phe	Thr	His	Pro	Gln
		180		185	
Leu	His				

<210> 274
 <211> 120
 <212> PRT
 <213> E. Coli

<400> 274	
Met	Leu
1	
Leu	Ile
Asn	Gln
Ser	Phe
Met	Arg
Val	Gly
Val	Thr
Phe	Ile

<210> 275
 <211> 306
 <212> PRT
 <213> E. Coli

<400> 275	
Met	Lys
1	
Pro	Ile
Glu	Val
Ser	Ile

50		55		60	
Ser Phe Thr Arg Asn Phe Gly Lys Glu Pro Ala Leu Phe Ala Gly Leu					
65		70		75	80
Asp His Ala Thr Gly Asp Ala Ile Ile Pro Ile Asp Val Asp Leu Gln					
	85		90		95
Asp Pro Ile Glu Val Ile Pro His Leu Ile Glu Lys Trp Gln Ala Gly					
	100		105		110
Ala Asp Met Val Leu Ala Lys Arg Ser Asp Arg Ser Thr Asp Gly Arg					
	115	120		125	
Leu Lys Arg Lys Thr Ala Glu Trp Phe Tyr Lys Leu His Asn Lys Ile					
	130	135		140	
Ser Asn Pro Lys Ile Glu Glu Asn Val Gly Asp Phe Arg Leu Met Ser					
145		150		155	160
Arg Asp Val Val Glu Asn Ile Lys Leu Met Pro Glu Arg Asn Leu Phe					
	165		170		175
Met Lys Gly Ile Leu Ser Trp Val Gly Gly Lys Thr Asp Ile Val Glu					
	180		185		190
Tyr Val Arg Ala Glu Arg Ile Ala Gly Asp Thr Lys Phe Asn Gly Trp					
	195	200		205	
Lys Leu Trp Asn Leu Ala Leu Glu Gly Ile Thr Ser Phe Ser Thr Phe					
	210	215		220	
Pro Leu Arg Ile Trp Thr Tyr Ile Gly Leu Val Val Ala Ser Val Ala					
225		230		235	240
Phe Ile Tyr Gly Ala Trp Met Ile Leu Asp Thr Ile Ile Phe Gly Asn					
	245		250		255
Ala Val Arg Gly Tyr Pro Ser Leu Leu Val Ser Ile Leu Phe Leu Gly					
	260	265		270	
Gly Ile Gln Met Ile Gly Ile Gly Val Leu Gly Glu Tyr Ile Gly Arg					
	275	280		285	
Thr Tyr Ile Glu Thr Lys Lys Arg Pro Lys Tyr Ile Ile Lys Arg Val					
	290	295		300	
Lys Lys					
305					

<210> 276
 <211> 443
 <212> PRT
 <213> E. Coli

<400> 276

Met Asn Lys Ala Ile Lys Val Ser Leu Tyr Ile Ser Phe Val Leu Ile	
1	5 10 15
Ile Cys Ala Leu Ser Lys Asn Ile Met Met Leu Asn Thr Ser Asp Phe	
	20 25 30
Gly Arg Ala Ile Lys Pro Leu Ile Glu Asp Ile Pro Ala Phe Thr Tyr	
	35 40 45
Asp Leu Pro Leu Leu Tyr Lys Leu Lys Gly His Ile Asp Ser Ile Asp	
	50 55 60
Ser Tyr Glu Tyr Ile Ser Ser Tyr Ser Tyr Ile Leu Tyr Thr Tyr Val	
65	70 75 80
Leu Phe Ile Ser Ile Phe Thr Glu Tyr Leu Asp Ala Arg Val Leu Ser	
	85 90 95
Leu Phe Leu Lys Val Ile Tyr Ile Tyr Ser Leu Tyr Ala Ile Phe Thr	
	100 105 110
Ser Tyr Ile Lys Thr Glu Arg Tyr Val Thr Leu Phe Thr Phe Phe Ile	
	115 120 125

Leu Ala Phe Leu Met Cys Ser Ser Ser Thr Leu Ser Met Phe Ala Ser
 130 135 140
 Phe Tyr Gln Glu Gln Ile Val Ile Ile Phe Leu Pro Phe Leu Val Tyr
 145 150 155 160
 Ser Leu Thr Cys Lys Asn Asn Lys Ser Met Leu Leu Leu Phe Phe Ser
 165 170 175
 Leu Leu Ile Ile Ser Thr Ala Lys Asn Gln Phe Ile Leu Thr Pro Leu
 180 185 190
 Ile Val Tyr Ser Tyr Tyr Ile Phe Phe Asp Arg His Lys Leu Ile Ile
 195 200 205
 Lys Ser Val Ile Cys Val Val Cys Leu Leu Ala Ser Ile Phe Ala Ile
 210 215 220
 Ser Tyr Ser Lys Gly Val Val Glu Leu Asn Lys Tyr His Ala Thr Tyr
 225 230 235 240
 Phe Gly Ser Tyr Leu Tyr Met Lys Asn Asn Gly Tyr Lys Met Pro Ser
 245 250 255
 Tyr Val Asp Asp Lys Cys Val Gly Leu Asp Ala Trp Gly Asn Lys Phe
 260 265 270
 Asp Ile Ser Phe Gly Ala Thr Pro Thr Glu Val Gly Thr Glu Cys Phe
 275 280 285
 Glu Ser His Lys Asp Glu Thr Phe Ser Asn Ala Leu Phe Leu Leu Val
 290 295 300
 Ser Lys Pro Ser Thr Ile Phe Lys Leu Pro Phe Asp Asp Gly Val Met
 305 310 315 320
 Ser Gln Tyr Lys Glu Asn Tyr Phe His Val Tyr Lys Lys Leu His Val
 325 330 335
 Ile Tyr Gly Glu Ser Asn Ile Leu Thr Thr Ile Thr Asn Ile Lys Asp
 340 345 350
 Asn Ile Phe Lys Asn Ile Arg Phe Ile Ser Leu Leu Leu Phe Phe Ile
 355 360 365
 Ala Ser Ile Phe Ile Arg Asn Asn Lys Ile Lys Ala Ser Leu Phe Val
 370 375 380
 Val Ser Leu Phe Gly Ile Ser Gln Phe Tyr Val Ser Phe Phe Gly Glu
 385 390 395 400
 Gly Tyr Arg Asp Leu Ser Lys His Leu Phe Gly Met Tyr Phe Ser Phe
 405 410 415
 Asp Leu Cys Leu Tyr Ile Thr Val Val Phe Leu Ile Tyr Lys Ile Ile
 420 425 430
 Gln Arg Asn Gln Asp Asn Ser Asp Val Lys His
 435 440

<210> 277

<211> 82

<212> PRT

<213> E. Coli

<400> 277

Met Gly Ile Leu Ser Trp Ile Ile Phe Gly Leu Ile Ala Gly Ile Leu
 1 5 10 15
 Ala Lys Trp Ile Met Pro Gly Lys Asp Gly Gly Gly Phe Phe Met Thr
 20 25 30
 Ile Leu Leu Gly Ile Val Gly Ala Val Val Gly Gly Trp Ile Ser Thr
 35 40 45
 Leu Phe Gly Phe Gly Lys Val Asp Gly Phe Asn Phe Gly Ser Phe Val
 50 55 60

Val Ala Val Ile Gly Ala Ile Val Val Leu Phe Ile Tyr Arg Lys Ile
 65 70 75 80
 Lys Ser

<210> 278
 <211> 60
 <212> PRT
 <213> E. Coli

<400> 278
 Met Gly Lys Ala Thr Tyr Thr Val Thr Val Thr Asn Asn Ser Asn Gly
 1 5 10 15
 Val Ser Val Asp Tyr Glu Thr Glu Thr Pro Met Thr Leu Leu Val Pro
 20 25 30
 Glu Val Ala Ala Glu Val Ile Lys Asp Leu Val Asn Thr Val Arg Ser
 35 40 45
 Tyr Asp Thr Glu Asn Glu His Asp Val Cys Gly Trp
 50 55 60

<210> 279
 <211> 119
 <212> PRT
 <213> E. Coli

<400> 279
 Met Leu Gln Ile Pro Gln Asn Tyr Ile His Thr Arg Ser Thr Pro Phe
 1 5 10 15
 Trp Asn Lys Gln Thr Ala Pro Ala Gly Ile Phe Glu Arg His Leu Asp
 20 25 30
 Lys Gly Thr Arg Pro Gly Val Tyr Pro Arg Leu Ser Val Met His Gly
 35 40 45
 Ala Val Lys Tyr Leu Gly Tyr Ala Asp Glu His Ser Ala Glu Pro Asp
 50 55 60
 Gln Val Ile Leu Ile Glu Ala Gly Gln Phe Ala Val Phe Pro Pro Glu
 65 70 75 80
 Lys Trp His Asn Ile Glu Ala Met Thr Asp Asp Thr Tyr Phe Asn Ile
 85 90 95
 Asp Phe Phe Val Ala Pro Glu Val Leu Met Glu Gly Ala Gln Gln Arg
 100 105 110
 Lys Val Ile His Asn Gly Lys
 115

<210> 280
 <211> 246
 <212> PRT
 <213> E. Coli

<400> 280
 Met Lys Phe Lys Val Ile Ala Leu Ala Ala Leu Met Gly Ile Ser Gly
 1 5 10 15
 Met Ala Ala Gln Ala Asn Glu Leu Pro Asp Gly Pro His Ile Val Thr
 20 25 30
 Ser Gly Thr Ala Ser Val Asp Ala Val Pro Asp Ile Ala Thr Leu Ala

Ala	Gln	Ala	Gln	Gly	Gln	Leu	Ala	Lys	Asp	Lys	Ala	Thr	Leu	Ala	Asn
			180					185					190		
Ala	Arg	Arg	Asp	Leu	Ala	Arg	Tyr	Gln	Gln	Leu	Ala	Lys	Thr	Asn	Leu
		195					200					205			
Val	Ser	Arg	Gln	Glu	Leu	Asp	Ala	Gln	Gln	Ala	Leu	Val	Ser	Glu	Thr
	210					215					220				
Glu	Gly	Thr	Ile	Lys	Ala	Asp	Glu	Ala	Ser	Val	Ala	Ser	Ala	Gln	Leu
225					230					235					240
Gln	Leu	Asp	Trp	Ser	Arg	Ile	Thr	Ala	Pro	Val	Asp	Gly	Arg	Val	Gly
			245						250					255	
Leu	Lys	Gln	Val	Asp	Val	Gly	Asn	Gln	Ile	Ser	Ser	Gly	Asp	Thr	Thr
			260					265					270		
Gly	Ile	Val	Val	Ile	Thr	Gln	Thr	His	Pro	Ile	Asp	Leu	Val	Phe	Thr
	275						280					285			
Leu	Pro	Glu	Ser	Asp	Ile	Ala	Thr	Val	Val	Gln	Ala	Gln	Lys	Ala	Gly
	290					295					300				
Lys	Pro	Leu	Val	Val	Glu	Ala	Trp	Asp	Arg	Thr	Asn	Ser	Lys	Lys	Leu
305					310					315					320
Ser	Glu	Gly	Thr	Leu	Leu	Ser	Leu	Asp	Asn	Gln	Ile	Asp	Ala	Thr	Thr
				325					330					335	
Gly	Thr	Ile	Lys	Val	Lys	Ala	Arg	Phe	Asn	Asn	Gln	Asp	Asp	Ala	Leu
			340					345					350		
Phe	Pro	Asn	Gln	Phe	Val	Asn	Ala	Arg	Met	Leu	Val	Asp	Thr	Glu	Gln
		355					360					365			
Asn	Ala	Val	Val	Ile	Pro	Thr	Ala	Ala	Leu	Gln	Met	Gly	Asn	Glu	Gly
	370					375					380				
His	Phe	Val	Trp	Val	Leu	Asn	Ser	Glu	Asn	Lys	Val	Ser	Lys	His	Leu
385					390					395					400
Val	Thr	Pro	Gly	Ile	Gln	Asp	Ser	Gln	Lys	Val	Val	Ile	Arg	Ala	Gly
				405					410					415	
Ile	Ser	Ala	Gly	Asp	Arg	Val	Val	Thr	Asp	Gly	Ile	Asp	Arg	Leu	Thr
			420					425					430		
Glu	Gly	Ala	Lys	Val	Glu	Val	Val	Glu	Ala	Gln	Ser	Ala	Thr	Thr	Pro
		435					440					445			
Glu	Glu	Lys	Ala	Thr	Ser	Arg	Glu	Tyr	Ala	Lys	Lys	Gly	Ala	Arg	Ser
	450					455					460				

<210> 282
 <211> 1040
 <212> PRT
 <213> E. Coli

<400> 282

Met	Gln	Val	Leu	Pro	Pro	Ser	Ser	Thr	Gly	Gly	Pro	Ser	Arg	Leu	Phe
1				5					10					15	
Ile	Met	Arg	Pro	Val	Ala	Thr	Thr	Leu	Leu	Met	Val	Ala	Ile	Leu	Leu
			20					25					30		
Ala	Gly	Ile	Ile	Gly	Tyr	Arg	Ala	Leu	Pro	Val	Ser	Ala	Leu	Pro	Glu
	35						40					45			
Val	Asp	Tyr	Pro	Thr	Ile	Gln	Val	Val	Thr	Leu	Tyr	Pro	Gly	Ala	Ser
	50					55					60				
Pro	Asp	Val	Met	Thr	Ser	Ala	Val	Thr	Ala	Pro	Leu	Glu	Arg	Gln	Phe
65					70					75				80	
Gly	Gln	Met	Ser	Gly	Leu	Lys	Gln	Met	Ser	Ser	Gln	Ser	Ser	Gly	Gly
				85					90					95	
Ala	Ser	Val	Ile	Thr	Leu	Gln	Phe	Gln	Leu	Thr	Leu	Pro	Leu	Asp	Val

1010	1015	1020
Leu Ala Leu Trp Thr	Lys Ser Arg Phe Ala Arg	His Glu Glu Glu Ala
1025	1030	1035 1040

<210> 283
 <211> 1025
 <212> PRT
 <213> E. Coli

<400> 283

Met	Lys	Phe	Phe	Ala	Leu	Phe	Ile	Tyr	Arg	Pro	Val	Ala	Thr	Ile	Leu
1				5					10					15	
Leu	Ser	Val	Ala	Ile	Thr	Leu	Cys	Gly	Ile	Leu	Gly	Phe	Arg	Met	Leu
			20					25					30		
Pro	Val	Ala	Pro	Leu	Pro	Gln	Val	Asp	Phe	Pro	Val	Ile	Ile	Val	Ser
		35					40					45			
Ala	Ser	Leu	Pro	Gly	Ala	Ser	Pro	Glu	Thr	Met	Ala	Ser	Ser	Val	Ala
	50					55					60				
Thr	Pro	Leu	Glu	Arg	Ser	Leu	Gly	Arg	Ile	Ala	Gly	Val	Ser	Glu	Met
65					70					75				80	
Thr	Ser	Ser	Ser	Ser	Leu	Gly	Ser	Thr	Arg	Ile	Ile	Leu	Gln	Phe	Asp
				85					90					95	
Phe	Asp	Arg	Asp	Ile	Asn	Gly	Ala	Ala	Arg	Asp	Val	Gln	Ala	Ala	Ile
			100					105					110		
Asn	Ala	Ala	Gln	Ser	Leu	Leu	Pro	Ser	Gly	Met	Pro	Ser	Arg	Pro	Thr
		115					120					125			
Tyr	Arg	Lys	Ala	Asn	Pro	Ser	Asp	Ala	Pro	Ile	Met	Ile	Leu	Thr	Leu
	130					135					140				
Thr	Ser	Asp	Thr	Tyr	Ser	Gln	Gly	Glu	Leu	Tyr	Asp	Phe	Ala	Ser	Thr
145					150					155					160
Gln	Leu	Ala	Pro	Thr	Ile	Ser	Gln	Ile	Asp	Gly	Val	Gly	Asp	Val	Asp
				165					170					175	
Val	Gly	Gly	Ser	Ser	Leu	Pro	Ala	Val	Arg	Val	Gly	Leu	Asn	Pro	Gln
			180					185					190		
Ala	Leu	Phe	Asn	Gln	Gly	Val	Ser	Leu	Asp	Asp	Val	Arg	Thr	Ala	Val
		195					200				205				
Ser	Asn	Ala	Asn	Val	Arg	Lys	Pro	Gln	Gly	Ala	Leu	Glu	Asp	Gly	Thr
	210					215					220				
His	Arg	Trp	Gln	Ile	Gln	Thr	Asn	Asp	Glu	Leu	Lys	Thr	Ala	Ala	Glu
225					230					235					240
Tyr	Gln	Pro	Leu	Ile	Ile	His	Tyr	Asn	Asn	Gly	Gly	Ala	Val	Arg	Leu
			245					250						255	
Gly	Asp	Val	Ala	Thr	Val	Thr	Asp	Ser	Val	Gln	Asp	Val	Arg	Asn	Ala
		260					265						270		
Gly	Met	Thr	Asn	Ala	Lys	Pro	Ala	Ile	Leu	Leu	Met	Ile	Arg	Lys	Leu
	275						280					285			
Pro	Glu	Ala	Asn	Ile	Ile	Gln	Thr	Val	Asp	Ser	Ile	Arg	Ala	Lys	Leu
	290					295					300				
Pro	Glu	Leu	Gln	Glu	Thr	Ile	Pro	Ala	Ala	Ile	Asp	Leu	Gln	Ile	Ala
305					310					315					320
Gln	Asp	Arg	Ser	Pro	Thr	Ile	Arg	Ala	Ser	Leu	Glu	Glu	Val	Glu	Gln
			325					330						335	
Thr	Leu	Ile	Ile	Ser	Val	Ala	Leu	Val	Ile	Leu	Val	Val	Phe	Leu	Phe
		340					345						350		
Leu	Arg	Ser	Gly	Arg	Ala	Thr	Ile	Ile	Pro	Ala	Val	Ser	Val	Pro	Val
		355				360						365			

Ser	Leu	Ile	Gly	Thr	Phe	Ala	Ala	Met	Tyr	Leu	Cys	Gly	Phe	Ser	Leu
370						375					380				
Asn	Asn	Leu	Ser	Leu	Met	Ala	Leu	Thr	Ile	Ala	Thr	Gly	Phe	Val	Val
385					390					395					400
Asp	Asp	Ala	Ile	Val	Val	Leu	Glu	Asn	Ile	Ala	Arg	His	Leu	Glu	Ala
				405					410					415	
Gly	Met	Lys	Pro	Leu	Gln	Ala	Ala	Leu	Gln	Gly	Thr	Arg	Glu	Val	Gly
			420					425					430		
Phe	Thr	Val	Leu	Ser	Met	Ser	Leu	Ser	Leu	Val	Ala	Val	Phe	Leu	Pro
		435					440					445			
Leu	Leu	Leu	Met	Gly	Gly	Leu	Pro	Gly	Arg	Leu	Leu	Arg	Glu	Phe	Ala
	450					455					460				
Val	Thr	Leu	Ser	Val	Ala	Ile	Gly	Ile	Ser	Leu	Leu	Val	Ser	Leu	Thr
465					470					475					480
Leu	Thr	Pro	Met	Met	Cys	Gly	Trp	Met	Leu	Lys	Ala	Ser	Lys	Pro	Arg
				485					490					495	
Glu	Gln	Lys	Arg	Leu	Arg	Gly	Phe	Gly	Arg	Met	Leu	Val	Ala	Leu	Gln
			500					505					510		
Gln	Gly	Tyr	Gly	Lys	Ser	Leu	Lys	Trp	Val	Leu	Asn	His	Thr	Arg	Leu
		515					520					525			
Val	Gly	Val	Val	Leu	Leu	Gly	Thr	Ile	Ala	Leu	Asn	Ile	Trp	Leu	Tyr
	530					535					540				
Ile	Ser	Ile	Pro	Lys	Thr	Phe	Phe	Pro	Glu	Gln	Asp	Thr	Gly	Val	Leu
545					550					555					560
Met	Gly	Gly	Ile	Gln	Ala	Asp	Gln	Ser	Ile	Ser	Phe	Gln	Ala	Met	Arg
				565					570					575	
Gly	Lys	Leu	Gln	Asp	Phe	Met	Lys	Ile	Ile	Arg	Asp	Asp	Pro	Ala	Val
			580					585					590		
Asp	Asn	Val	Thr	Gly	Phe	Thr	Gly	Gly	Ser	Arg	Val	Asn	Ser	Gly	Met
		595					600					605			
Met	Phe	Ile	Thr	Leu	Lys	Pro	Arg	Asp	Glu	Arg	Ser	Glu	Thr	Ala	Gln
	610					615					620				
Gln	Ile	Ile	Asp	Arg	Leu	Arg	Val	Lys	Leu	Ala	Lys	Glu	Pro	Gly	Ala
625					630					635					640
Asn	Leu	Phe	Leu	Met	Ala	Val	Gln	Asp	Ile	Arg	Val	Gly	Gly	Arg	Gln
				645					650					655	
Ser	Asn	Ala	Ser	Tyr	Gln	Tyr	Thr	Leu	Leu	Ser	Asp	Asp	Leu	Ala	Ala
		660						665					670		
Leu	Arg	Glu	Trp	Glu	Pro	Lys	Ile	Arg	Lys	Lys	Leu	Ala	Thr	Leu	Pro
		675				680						685			
Glu	Leu	Ala	Asp	Val	Asn	Ser	Asp	Gln	Gln	Asp	Asn	Gly	Ala	Glu	Met
	690					695					700				
Asn	Leu	Val	Tyr	Asp	Arg	Asp	Thr	Met	Ala	Arg	Leu	Gly	Ile	Asp	Val
705					710					715					720
Gln	Ala	Ala	Asn	Ser	Leu	Leu	Asn	Asn	Ala	Phe	Gly	Gln	Arg	Gln	Ile
				725					730					735	
Ser	Thr	Ile	Tyr	Gln	Pro	Met	Asn	Gln	Tyr	Lys	Val	Val	Met	Glu	Val
			740					745					750		
Asp	Pro	Arg	Tyr	Thr	Gln	Asp	Ile	Ser	Ala	Leu	Glu	Lys	Met	Phe	Val
		755					760					765			
Ile	Asn	Asn	Glu	Gly	Lys	Ala	Ile	Pro	Leu	Ser	Tyr	Phe	Ala	Lys	Trp
	770					775					780				
Gln	Pro	Ala	Asn	Ala	Pro	Leu	Ser	Val	Asn	His	Gln	Gly	Leu	Ser	Ala
785					790					795					800
Ala	Ser	Thr	Ile	Ser	Phe	Asn	Leu	Pro	Thr	Gly	Lys	Ser	Leu	Ser	Asp
				805					810					815	
Ala	Ser	Ala	Ala	Ile	Asp	Arg	Ala	Met	Thr	Gln	Leu	Gly	Val	Pro	Ser

Gly	Ala	Ile	Ala	Thr	Leu	Leu	Leu	Met	Pro	Asn	Tyr	Thr	Met	Gln	Thr
			180					185					190		
Arg	Arg	Phe	Asp	Leu	Ser	Gly	Phe	Leu	Leu	Leu	Ala	Val	Gly	Met	Ala
		195					200					205			
Val	Leu	Thr	Leu	Ala	Leu	Asp	Gly	Ser	Lys	Gly	Thr	Gly	Leu	Ser	Pro
	210					215					220				
Leu	Thr	Ile	Ala	Gly	Leu	Val	Ala	Val	Gly	Val	Val	Ala	Leu	Val	Leu
225					230					235					240
Tyr	Leu	Leu	His	Ala	Arg	Asn	Asn	Asn	Arg	Ala	Leu	Phe	Ser	Leu	Lys
			245						250					255	
Leu	Phe	Arg	Thr	Arg	Thr	Phe	Ser	Leu	Gly	Leu	Ala	Gly	Ser	Phe	Ala
			260					265					270		
Gly	Arg	Ile	Gly	Ser	Gly	Met	Leu	Pro	Phe	Met	Thr	Pro	Val	Phe	Leu
		275					280					285			
Gln	Ile	Gly	Leu	Gly	Phe	Ser	Pro	Phe	His	Ala	Gly	Leu	Met	Met	Ile
	290					295					300				
Pro	Met	Val	Leu	Gly	Ser	Met	Gly	Met	Lys	Arg	Ile	Val	Val	Gln	Val
305					310					315					320
Val	Asn	Arg	Phe	Gly	Tyr	Arg	Arg	Val	Leu	Val	Ala	Thr	Thr	Leu	Gly
				325					330					335	
Leu	Ser	Leu	Val	Thr	Leu	Leu	Phe	Met	Thr	Thr	Ala	Leu	Leu	Gly	Trp
			340					345					350		
Tyr	Tyr	Val	Leu	Pro	Phe	Val	Leu	Phe	Leu	Gln	Gly	Met	Val	Asn	Ser
		355					360					365			
Thr	Arg	Phe	Ser	Ser	Met	Asn	Thr	Leu	Thr	Leu	Lys	Asp	Leu	Pro	Asp
	370					375					380				
Asn	Leu	Ala	Ser	Ser	Gly	Asn	Ser	Leu	Leu	Ser	Met	Ile	Met	Gln	Leu
385					390					395					400
Ser	Met	Ser	Ile	Gly	Val	Thr	Ile	Ala	Gly	Leu	Leu	Leu	Gly	Leu	Phe
				405					410					415	
Gly	Ser	Gln	His	Val	Ser	Val	Asp	Ser	Gly	Thr	Thr	Gln	Thr	Val	Phe
			420					425					430		
Met	Tyr	Thr	Trp	Leu	Ser	Met	Ala	Leu	Ile	Ile	Ala	Leu	Pro	Ala	Phe
		435					440					445			
Ile	Phe	Ala	Arg	Val	Pro	Asn	Asp	Thr	His	Gln	Asn	Val	Ala	Ile	Ser
	450					455					460				
Arg	Arg	Lys	Arg	Ser	Ala	Gln									
465					470										

<210> 285
 <211> 344
 <212> PRT
 <213> E. Coli

<400> 285

Met	Glu	Ile	Arg	Ile	Met	Leu	Phe	Ile	Leu	Met	Met	Met	Val	Met	Pro
1				5					10				15		
Val	Ser	Tyr	Ala	Ala	Cys	Tyr	Ser	Glu	Leu	Ser	Val	Gln	His	Asn	Leu
			20					25				30			
Val	Val	Gln	Gly	Asp	Phe	Ala	Leu	Thr	Gln	Thr	Gln	Met	Ala	Thr	Tyr
		35					40					45			
Glu	His	Asn	Phe	Asn	Asp	Ser	Ser	Cys	Val	Ser	Thr	Asn	Thr	Ile	Thr
	50					55					60				
Pro	Met	Ser	Pro	Ser	Asp	Ile	Ile	Val	Gly	Leu	Tyr	Asn	Asp	Thr	Ile
65					70					75					80
Lys	Leu	Asn	Leu	His	Phe	Glu	Trp	Thr	Asn	Lys	Asn	Asn	Ile	Thr	Leu

85 90 95
 Ser Asn Asn Gln Thr Ser Phe Thr Ser Gly Tyr Ser Val Thr Val Thr
 100 105 110
 Pro Ala Ala Ser Asn Ala Lys Val Asn Val Ser Ala Gly Gly Gly Gly
 115 120 125
 Ser Val Met Ile Asn Gly Val Ala Thr Leu Ser Ser Ala Ser Ser Ser
 130 135 140
 Thr Arg Gly Ser Ala Ala Val Gln Phe Leu Leu Cys Leu Leu Gly Gly
 145 150 155 160
 Lys Ser Trp Asp Ala Cys Val Asn Ser Tyr Arg Asn Ala Leu Ala Gln
 165 170 175
 Asn Ala Gly Val Tyr Ser Phe Asn Leu Thr Leu Ser Tyr Asn Pro Ile
 180 185 190
 Thr Thr Thr Cys Lys Pro Asp Asp Leu Leu Ile Thr Leu Asp Ser Ile
 195 200 205
 Pro Val Ser Gln Leu Pro Ala Thr Gly Asn Lys Ala Thr Ile Asn Ser
 210 215 220
 Lys Gln Gly Asp Ile Ile Leu Arg Cys Lys Asn Leu Leu Gly Gln Gln
 225 230 235 240
 Asn Gln Thr Ser Arg Lys Met Gln Val Tyr Leu Ser Ser Ser Asp Leu
 245 250 255
 Leu Thr Asn Ser Asn Thr Ile Leu Lys Gly Ala Glu Asp Asn Gly Val
 260 265 270
 Gly Phe Ile Leu Glu Ser Asn Gly Ser Pro Val Thr Leu Leu Asn Ile
 275 280 285
 Thr Asn Ser Ser Lys Gly Tyr Thr Asn Leu Lys Glu Val Ala Ala Lys
 290 295 300
 Ser Lys Leu Thr Asp Thr Thr Val Ser Ile Pro Ile Thr Ala Ser Tyr
 305 310 315 320
 Tyr Val Tyr Asp Thr Asn Lys Val Lys Ser Gly Ala Leu Glu Ala Thr
 325 330 335
 Ala Leu Ile Asn Val Lys Tyr Asp
 340

<210> 286
 <211> 826
 <212> PRT
 <213> E. Coli

<400> 286
 Met Leu Arg Met Thr Pro Leu Ala Ser Ala Ile Val Ala Leu Leu Leu
 1 5 10 15
 Gly Ile Glu Ala Tyr Ala Ala Glu Glu Thr Phe Asp Thr His Phe Met
 20 25 30
 Ile Gly Gly Met Lys Asp Gln Gln Val Ala Asn Ile Arg Leu Asp Asp
 35 40 45
 Asn Gln Pro Leu Pro Gly Gln Tyr Asp Ile Asp Ile Tyr Val Asn Lys
 50 55 60
 Gln Trp Arg Gly Lys Tyr Glu Ile Ile Val Lys Asp Asn Pro Gln Glu
 65 70 75 80
 Thr Cys Leu Ser Arg Glu Val Ile Lys Arg Leu Gly Ile Asn Ser Asp
 85 90 95
 Asn Phe Ala Ser Gly Lys Gln Cys Leu Thr Phe Glu Gln Leu Val Gln
 100 105 110
 Gly Gly Ser Tyr Thr Trp Asp Ile Gly Val Phe Arg Leu Asp Phe Ser
 115 120 125

Val Pro Gln Ala Trp Val Glu Glu Leu Glu Ser Gly Tyr Val Pro Pro
 130 135 140
 Glu Asn Trp Glu Arg Gly Ile Asn Ala Phe Tyr Thr Ser Tyr Tyr Leu
 145 150 155 160
 Ser Gln Tyr Tyr Ser Asp Tyr Lys Ala Ser Gly Asn Asn Lys Ser Thr
 165 170 175
 Tyr Val Arg Phe Asn Ser Gly Leu Asn Leu Leu Gly Trp Gln Leu His
 180 185 190
 Ser Asp Ala Ser Phe Ser Lys Thr Asn Asn Asn Pro Gly Val Trp Lys
 195 200 205
 Ser Asn Thr Leu Tyr Leu Glu Arg Gly Phe Ala Gln Leu Leu Gly Thr
 210 215 220
 Leu Arg Val Gly Asp Met Tyr Thr Ser Ser Asp Ile Phe Asp Ser Val
 225 230 235 240
 Arg Phe Arg Gly Val Arg Leu Phe Arg Asp Met Gln Met Leu Pro Asn
 245 250 255
 Ser Lys Gln Asn Phe Thr Pro Arg Val Gln Gly Ile Ala Gln Ser Asn
 260 265 270
 Ala Leu Val Thr Ile Glu Gln Asn Gly Phe Val Val Tyr Gln Lys Glu
 275 280 285
 Val Pro Pro Gly Pro Phe Ala Ile Thr Asp Leu Gln Leu Ala Gly Gly
 290 295 300
 Gly Ala Asp Leu Asp Val Ser Val Lys Glu Ala Asp Gly Ser Val Thr
 305 310 315 320
 Thr Tyr Leu Val Pro Tyr Ala Ala Val Pro Asn Met Leu Gln Pro Gly
 325 330 335
 Val Ser Lys Tyr Asp Leu Ala Ala Gly Arg Ser His Ile Glu Gly Ala
 340 345 350
 Ser Lys Gln Ser Asp Phe Val Gln Ala Gly Tyr Gln Tyr Gly Phe Asn
 355 360 365
 Asn Leu Leu Thr Leu Tyr Gly Gly Ser Met Val Ala Asn Asn Tyr Tyr
 370 375 380
 Ala Phe Thr Leu Gly Ala Gly Trp Asn Thr Arg Ile Gly Ala Ile Ser
 385 390 395 400
 Val Asp Ala Thr Lys Ser His Ser Lys Gln Asp Asn Gly Asp Val Phe
 405 410 415
 Asp Gly Gln Ser Tyr Gln Ile Ala Tyr Asn Lys Phe Val Ser Gln Thr
 420 425 430
 Ser Thr Arg Phe Gly Leu Ala Ala Trp Arg Tyr Ser Ser Arg Asp Tyr
 435 440 445
 Arg Thr Phe Asn Asp His Val Trp Ala Asn Asn Lys Asp Asn Tyr Arg
 450 455 460
 Arg Asp Glu Asn Asp Val Tyr Asp Ile Ala Asp Tyr Tyr Gln Asn Asp
 465 470 475 480
 Phe Gly Arg Lys Asn Ser Phe Ser Ala Asn Met Ser Gln Ser Leu Pro
 485 490 495
 Glu Gly Trp Gly Ser Val Ser Leu Ser Thr Leu Trp Arg Asp Tyr Trp
 500 505 510
 Gly Arg Ser Gly Ser Ser Lys Asp Tyr Gln Leu Ser Tyr Ser Asn Asn
 515 520 525
 Leu Arg Arg Ile Ser Tyr Thr Leu Ala Ala Ser Gln Ala Tyr Asp Glu
 530 535 540
 Asn His His Glu Glu Lys Arg Phe Asn Ile Phe Ile Ser Ile Pro Phe
 545 550 555 560
 Asp Trp Gly Asp Asp Val Ser Thr Pro Arg Arg Gln Ile Tyr Met Ser
 565 570 575
 Asn Ser Thr Thr Phe Asp Asp Gln Gly Phe Ala Ser Asn Asn Thr Gly

Asn	Arg	Ile	Lys	Leu	Phe	Tyr	Arg	Pro	Ala	Gly	Ile	Ala	Pro	Val	Asn
145					150					155					160
Lys	Ala	Thr	Phe	Lys	Lys	Leu	Leu	Val	Asn	Arg	Ser	Gly	Asn	Gly	Leu
			165						170					175	
Val	Ile	Lys	Asn	Asp	Ser	Ala	Asn	Trp	Val	Thr	Ile	Ser	Asp	Val	Lys
			180					185					190		
Ala	Asn	Asn	Val	Lys	Val	Asn	Tyr	Glu	Thr	Ile	Met	Ile	Ala	Pro	Leu
		195					200					205			
Glu	Ser	Gln	Ser	Val	Asn	Val	Lys	Ser	Asn	Asn	Ala	Asn	Asn	Trp	His
	210					215					220				
Leu	Thr	Ile	Ile	Asp	Asp	His	Gly	Asn	Tyr	Ile	Ser	Asp	Lys	Ile	
225					230					235					

<210> 288
 <211> 180
 <212> PRT
 <213> E. Coli

<400> 288

Met	Lys	Arg	Ser	Ile	Ile	Ala	Ala	Ala	Val	Phe	Ser	Ser	Phe	Phe	Met
1				5					10					15	
Ser	Ala	Gly	Val	Phe	Ala	Ala	Asp	Val	Asp	Thr	Gly	Thr	Leu	Thr	Ile
			20				25						30		
Lys	Gly	Asn	Ile	Ala	Glu	Ser	Pro	Cys	Lys	Phe	Glu	Ala	Gly	Gly	Asp
		35					40					45			
Ser	Val	Ser	Ile	Asn	Met	Pro	Thr	Val	Pro	Thr	Ser	Val	Phe	Glu	Gly
	50					55					60				
Lys	Ala	Lys	Tyr	Ser	Thr	Tyr	Asp	Asp	Ala	Val	Gly	Val	Thr	Ser	Ser
	65				70					75					80
Met	Leu	Lys	Ile	Ser	Cys	Pro	Lys	Glu	Val	Ala	Gly	Val	Lys	Leu	Ser
				85					90					95	
Leu	Ile	Thr	Asn	Asp	Lys	Ile	Thr	Gly	Asn	Asp	Lys	Ala	Ile	Ala	Ser
			100					105					110		
Ser	Asn	Asp	Thr	Val	Gly	Tyr	Tyr	Leu	Tyr	Leu	Gly	Asp	Asn	Ser	Asp
		115					120					125			
Val	Leu	Asp	Val	Ser	Ala	Pro	Phe	Asn	Ile	Glu	Ser	Tyr	Lys	Thr	Ala
	130					135						140			
Glu	Gly	Gln	Tyr	Ala	Ile	Pro	Phe	Lys	Ala	Lys	Tyr	Leu	Lys	Leu	Thr
	145				150					155					160
Asp	Asn	Ser	Val	Gln	Ser	Gly	Asp	Val	Leu	Ser	Ser	Leu	Val	Met	Arg
				165					170					175	
Val	Ala	Gln	Asp												
			180												

<210> 289
 <211> 112
 <212> PRT
 <213> E. Coli

<400> 289

Met	Ser	Ser	Glu	Arg	Asp	Leu	Val	Asn	Phe	Leu	Gly	Asp	Phe	Ser	Met
1				5					10					15	
Asp	Val	Ala	Lys	Ala	Val	Ile	Ala	Gly	Gly	Val	Ala	Thr	Ala	Ile	Gly
			20						25					30	

Ser	Leu	Ala	Ser	Phe	Ala	Cys	Val	Ser	Phe	Gly	Phe	Pro	Val	Ile	Leu
		35					40					45			
Val	Gly	Gly	Ala	Ile	Leu	Leu	Thr	Gly	Ile	Val	Cys	Thr	Val	Val	Leu
	50					55					60				
Asn	Glu	Ile	Asp	Ala	Gln	Cys	His	Leu	Ser	Glu	Lys	Leu	Lys	Tyr	Ala
65					70					75					80
Ile	Arg	Asp	Gly	Leu	Lys	Arg	Gln	Gln	Glu	Leu	Asp	Lys	Trp	Lys	Arg
				85					90					95	
Glu	Asn	Met	Thr	Pro	Phe	Met	Tyr	Val	Leu	Asn	Thr	Pro	Pro	Val	Ile
			100					105					110		

<210> 290
 <211> 193
 <212> PRT
 <213> E. Coli

<400> 290															
Met	Thr	Asp	Tyr	Leu	Leu	Leu	Phe	Val	Gly	Thr	Val	Leu	Val	Asn	Asn
1				5					10					15	
Phe	Val	Leu	Val	Lys	Phe	Leu	Gly	Leu	Cys	Pro	Phe	Met	Gly	Val	Ser
		20					25						30		
Lys	Lys	Leu	Glu	Thr	Ala	Met	Gly	Met	Gly	Leu	Ala	Thr	Thr	Phe	Val
		35					40					45			
Met	Thr	Leu	Ala	Ser	Ile	Cys	Ala	Trp	Leu	Ile	Asp	Thr	Trp	Ile	Leu
	50					55					60				
Ile	Pro	Leu	Asn	Leu	Ile	Tyr	Leu	Arg	Thr	Leu	Ala	Phe	Ile	Leu	Val
65				70					75						80
Ile	Ala	Val	Val	Val	Gln	Phe	Thr	Glu	Met	Val	Val	Arg	Lys	Thr	Ser
				85					90					95	
Pro	Val	Leu	Tyr	Arg	Leu	Leu	Gly	Ile	Phe	Leu	Pro	Leu	Ile	Thr	Thr
			100					105					110		
Asn	Cys	Ala	Val	Leu	Gly	Val	Ala	Leu	Leu	Asn	Ile	Asn	Leu	Gly	His
		115					120					125			
Asn	Phe	Leu	Gln	Ser	Ala	Leu	Tyr	Gly	Phe	Ser	Ala	Ala	Val	Gly	Phe
	130					135					140				
Ser	Leu	Val	Met	Val	Leu	Phe	Ala	Ala	Ile	Arg	Glu	Arg	Leu	Ala	Val
145					150					155					160
Ala	Asp	Val	Pro	Ala	Pro	Phe	Arg	Gly	Asn	Ala	Ile	Ala	Leu	Ile	Thr
				165				170						175	
Ala	Gly	Leu	Met	Ser	Leu	Ala	Phe	Met	Gly	Phe	Ser	Gly	Leu	Val	Lys
			180					185					190		
Leu															

<210> 291
 <211> 192
 <212> PRT
 <213> E. Coli

<400> 291															
Met	Asn	Ala	Ile	Trp	Ile	Ala	Val	Ala	Ala	Val	Ser	Leu	Leu	Gly	Leu
1				5					10					15	
Ala	Phe	Gly	Ala	Ile	Leu	Gly	Tyr	Ala	Ser	Arg	Arg	Phe	Ala	Val	Glu
		20						25					30		

Asp	Asp	Pro	Val	Val	Glu	Lys	Ile	Asp	Glu	Ile	Leu	Pro	Gln	Ser	Gln
	35						40					45			
Cys	Gly	Gln	Cys	Gly	Tyr	Pro	Gly	Cys	Arg	Pro	Tyr	Ala	Glu	Ala	Ile
	50					55					60				
Ser	Cys	Asn	Gly	Glu	Lys	Ile	Asn	Arg	Cys	Ala	Pro	Gly	Gly	Glu	Ala
65					70				75						80
Val	Met	Leu	Lys	Ile	Ala	Glu	Leu	Leu	Asn	Val	Glu	Pro	Gln	Pro	Leu
			85						90					95	
Asp	Gly	Glu	Ala	Gln	Glu	Ile	Thr	Pro	Ala	Arg	Met	Val	Ala	Val	Ile
			100					105					110		
Asp	Glu	Asn	Asn	Cys	Ile	Gly	Cys	Thr	Lys	Cys	Ile	Gln	Ala	Cys	Pro
	115						120					125			
Val	Asp	Ala	Ile	Val	Gly	Ala	Thr	Arg	Ala	Met	His	Thr	Val	Met	Ser
	130					135					140				
Asp	Leu	Cys	Thr	Gly	Cys	Asn	Leu	Cys	Val	Asp	Pro	Cys	Pro	Thr	His
145					150				155						160
Cys	Ile	Ser	Leu	Gln	Pro	Val	Ala	Glu	Thr	Pro	Asp	Ser	Trp	Lys	Trp
				165					170					175	
Asp	Leu	Asn	Thr	Ile	Pro	Val	Arg	Ile	Ile	Pro	Val	Glu	His	His	Ala
			180					185					190		

<210> 292
 <211> 740
 <212> PRT
 <213> E. Coli

<400> 292

Met	Leu	Lys	Leu	Phe	Ser	Ala	Phe	Arg	Lys	Asn	Lys	Ile	Trp	Asp	Phe
1				5					10					15	
Asn	Gly	Gly	Ile	His	Pro	Pro	Glu	Met	Lys	Thr	Gln	Ser	Asn	Gly	Thr
			20					25					30		
Pro	Leu	Arg	Gln	Val	Pro	Leu	Ala	Gln	Arg	Phe	Val	Ile	Pro	Leu	Lys
		35					40					45			
Gln	His	Ile	Gly	Ala	Glu	Gly	Glu	Leu	Cys	Val	Ser	Val	Gly	Asp	Lys
	50					55					60				
Val	Leu	Arg	Gly	Gln	Pro	Leu	Thr	Arg	Gly	Arg	Gly	Lys	Met	Leu	Pro
65					70				75						80
Val	His	Ala	Pro	Thr	Ser	Gly	Thr	Val	Thr	Ala	Ile	Ala	Pro	His	Ser
				85					90					95	
Thr	Ala	His	Pro	Ser	Ala	Leu	Ala	Glu	Leu	Ser	Val	Ile	Ile	Asp	Ala
			100					105					110		
Asp	Gly	Glu	Asp	Cys	Trp	Ile	Pro	Arg	Asp	Gly	Trp	Ala	Asp	Tyr	Arg
	115						120					125			
Thr	Arg	Ser	Arg	Glu	Glu	Leu	Ile	Glu	Arg	Ile	His	Gln	Phe	Gly	Val
	130					135					140				
Ala	Gly	Leu	Gly	Gly	Ala	Gly	Phe	Pro	Thr	Gly	Val	Lys	Leu	Gln	Gly
145					150					155					160
Gly	Gly	Asp	Lys	Ile	Glu	Thr	Leu	Ile	Ile	Asn	Ala	Ala	Glu	Cys	Glu
				165					170					175	
Pro	Tyr	Ile	Thr	Ala	Asp	Asp	Arg	Leu	Met	Gln	Asp	Cys	Ala	Ala	Gln
			180					185					190		
Val	Val	Glu	Gly	Ile	Arg	Ile	Leu	Ala	His	Ile	Leu	Gln	Pro	Arg	Glu
	195						200					205			
Ile	Leu	Ile	Gly	Ile	Glu	Asp	Asn	Lys	Pro	Gln	Ala	Ile	Ser	Met	Leu
	210					215					220				
Arg	Ala	Val	Leu	Ala	Asp	Ser	Asn	Asp	Ile	Ser	Leu	Arg	Val	Ile	Pro

225					230					235					240
Thr	Lys	Tyr	Pro	Ser	Gly	Gly	Ala	Lys	Gln	Leu	Thr	Tyr	Ile	Leu	Thr
				245					250					255	
Gly	Lys	Gln	Val	Pro	His	Gly	Gly	Arg	Ser	Ser	Asp	Ile	Gly	Val	Leu
			260					265					270		
Met	Gln	Asn	Val	Gly	Thr	Ala	Tyr	Ala	Val	Lys	Arg	Ala	Val	Ile	Asp
		275					280					285			
Gly	Glu	Pro	Ile	Thr	Glu	Arg	Val	Val	Thr	Leu	Thr	Gly	Glu	Ala	Ile
	290					295				300					
Ala	Arg	Pro	Gly	Asn	Val	Trp	Ala	Arg	Leu	Gly	Thr	Pro	Val	Arg	His
305				310					315						320
Leu	Leu	Asn	Asp	Ala	Gly	Phe	Cys	Pro	Ser	Ala	Asp	Gln	Met	Val	Ile
			325						330					335	
Met	Gly	Gly	Pro	Leu	Met	Gly	Phe	Thr	Leu	Pro	Trp	Leu	Asp	Val	Pro
			340					345					350		
Val	Val	Lys	Ile	Thr	Asn	Cys	Leu	Leu	Ala	Pro	Ser	Ala	Asn	Glu	Leu
		355				360						365			
Gly	Glu	Pro	Gln	Glu	Glu	Gln	Ser	Cys	Ile	Arg	Cys	Ser	Ala	Cys	Ala
	370					375					380				
Asp	Ala	Cys	Pro	Ala	Asp	Leu	Leu	Pro	Gln	Gln	Leu	Tyr	Trp	Phe	Ser
385					390				395						400
Lys	Gly	Gln	Gln	His	Asp	Lys	Ala	Thr	Thr	His	Asn	Ile	Ala	Asp	Cys
				405					410					415	
Ile	Glu	Cys	Gly	Ala	Cys	Ala	Trp	Val	Cys	Pro	Ser	Asn	Ile	Pro	Leu
			420					425					430		
Val	Gln	Tyr	Phe	Arg	Gln	Glu	Lys	Ala	Glu	Ile	Ala	Ala	Ile	Arg	Gln
		435					440					445			
Glu	Glu	Lys	Arg	Ala	Ala	Glu	Ala	Lys	Ala	Arg	Phe	Glu	Ala	Arg	Gln
	450					455					460				
Ala	Arg	Leu	Glu	Arg	Glu	Lys	Ala	Ala	Arg	Leu	Glu	Arg	His	Lys	Ser
465				470					475						480
Ala	Ala	Val	Gln	Pro	Ala	Ala	Lys	Asp	Lys	Asp	Ala	Ile	Ala	Ala	Ala
			485					490						495	
Leu	Ala	Arg	Val	Lys	Glu	Lys	Gln	Ala	Gln	Ala	Thr	Gln	Pro	Ile	Val
			500				505						510		
Ile	Lys	Ala	Gly	Glu	Arg	Pro	Asp	Asn	Ser	Ala	Ile	Ile	Ala	Ala	Arg
	515					520						525			
Glu	Ala	Arg	Lys	Ala	Gln	Ala	Arg	Ala	Lys	Gln	Ala	Glu	Leu	Gln	Gln
	530				535					540					
Thr	Asn	Asp	Ala	Ala	Thr	Val	Ala	Asp	Pro	Arg	Lys	Thr	Ala	Val	Glu
545				550					555						560
Ala	Ala	Ile	Ala	Arg	Ala	Lys	Ala	Arg	Lys	Leu	Glu	Gln	Gln	Gln	Ala
			565					570						575	
Asn	Ala	Glu	Pro	Glu	Gln	Gln	Val	Asp	Pro	Arg	Lys	Ala	Ala	Val	Glu
		580					585						590		
Ala	Ala	Ile	Ala	Arg	Ala	Lys	Ala	Arg	Lys	Leu	Glu	Gln	Gln	Gln	Ala
	595					600						605			
Asn	Ala	Glu	Pro	Glu	Glu	Gln	Val	Asp	Pro	Arg	Lys	Ala	Ala	Val	Glu
	610				615				620						
Ala	Ala	Ile	Ala	Arg	Ala	Lys	Ala	Arg	Lys	Leu	Glu	Gln	Gln	Gln	Ala
625				630					635						640
Asn	Ala	Glu	Pro	Glu	Gln	Gln	Val	Asp	Pro	Arg	Lys	Ala	Ala	Val	Glu
			645				650						655		
Ala	Ala	Ile	Ala	Arg	Ala	Lys	Ala	Arg	Lys	Arg	Glu	Gln	Gln	Pro	Ala
	660					665						670			
Asn	Ala	Glu	Pro	Glu	Glu	Gln	Val	Asp	Pro	Arg	Lys	Ala	Ala	Val	Glu
	675				680							685			

Ala	Ala	Ile	Ala	Arg	Ala	Lys	Ala	Arg	Lys	Leu	Glu	Gln	Gln	Gln	Ala
690						695					700				
Asn	Ala	Val	Pro	Glu	Glu	Gln	Val	Asp	Pro	Arg	Lys	Ala	Ala	Val	Ala
705					710					715					720
Ala	Ala	Ile	Ala	Arg	Ala	Gln	Ala	Lys	Lys	Ala	Ala	Gln	Gln	Lys	Val
				725					730					735	
Val	Asn	Glu	Asp												
			740												

<210> 293
 <211> 352
 <212> PRT
 <213> E. Coli

<400> 293															
Met	Val	Phe	Arg	Ile	Ala	Ser	Ser	Pro	Tyr	Thr	His	Asn	Gln	Arg	Gln
1				5					10					15	
Thr	Ser	Arg	Ile	Met	Leu	Leu	Val	Leu	Leu	Ala	Ala	Val	Pro	Gly	Ile
			20					25					30		
Ala	Ala	Gln	Leu	Trp	Phe	Phe	Gly	Trp	Gly	Thr	Leu	Val	Gln	Ile	Leu
		35					40					45			
Leu	Ala	Ser	Val	Ser	Ala	Leu	Leu	Ala	Glu	Ala	Leu	Val	Leu	Lys	Leu
	50					55					60				
Arg	Lys	Gln	Ser	Val	Ala	Ala	Thr	Leu	Lys	Asp	Asn	Ser	Ala	Leu	Leu
65					70					75					80
Thr	Gly	Leu	Leu	Leu	Ala	Val	Ser	Ile	Pro	Pro	Leu	Ala	Pro	Trp	Trp
				85					90					95	
Met	Val	Val	Leu	Gly	Thr	Val	Phe	Ala	Val	Ile	Ile	Ala	Lys	Gln	Leu
			100					105					110		
Tyr	Gly	Gly	Leu	Gly	Gln	Asn	Pro	Phe	Asn	Pro	Ala	Met	Ile	Gly	Tyr
		115				120					125				
Val	Val	Leu	Leu	Ile	Ser	Phe	Pro	Val	Gln	Met	Thr	Ser	Trp	Leu	Pro
	130					135					140				
Pro	His	Glu	Ile	Ala	Val	Asn	Ile	Pro	Gly	Phe	Ile	Asp	Ala	Ile	Gln
				150						155					160
Val	Ile	Phe	Ser	Gly	His	Thr	Ala	Ser	Gly	Gly	Asp	Met	Asn	Thr	Leu
				165					170					175	
Arg	Leu	Gly	Ile	Asp	Gly	Ile	Ser	Gln	Ala	Thr	Pro	Leu	Asp	Thr	Phe
		180						185					190		
Lys	Thr	Ser	Val	Arg	Ala	Gly	His	Ser	Val	Glu	Gln	Ile	Met	Gln	Tyr
		195					200					205			
Pro	Ile	Tyr	Ser	Gly	Ile	Leu	Ala	Gly	Ala	Gly	Trp	Gln	Trp	Val	Asn
	210					215					220				
Leu	Ala	Trp	Leu	Ala	Gly	Gly	Val	Trp	Leu	Leu	Trp	Gln	Lys	Ala	Ile
	225				230				235						240
Arg	Trp	His	Ile	Pro	Leu	Ser	Phe	Leu	Val	Thr	Leu	Ala	Leu	Cys	Ala
				245					250					255	
Met	Leu	Gly	Trp	Leu	Phe	Ser	Pro	Glu	Thr	Leu	Ala	Ala	Pro	Gln	Ile
		260						265					270		
His	Leu	Leu	Ser	Gly	Ala	Thr	Met	Leu	Gly	Ala	Phe	Phe	Ile	Leu	Thr
		275					280					285			
Asp	Pro	Val	Thr	Ala	Ser	Thr	Thr	Asn	Arg	Gly	Arg	Leu	Ile	Phe	Gly
	290					295					300				
Ala	Leu	Ala	Gly	Leu	Leu	Val	Trp	Leu	Ile	Arg	Ser	Phe	Gly	Gly	Tyr
	305				310					315					320

Pro	Asp	Gly	Val	Ala	Phe	Ala	Val	Leu	Leu	Ala	Asn	Ile	Thr	Val	Pro
				325					330					335	
Leu	Ile	Asp	Tyr	Tyr	Thr	Arg	Pro	Arg	Val	Tyr	Gly	His	Arg	Lys	Gly
			340					345					350		

<210> 294
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 <212> PRT
 <213> E. Coli

<400> 294															
Met	Leu	Lys	Thr	Ile	Arg	Lys	His	Gly	Ile	Thr	Leu	Ala	Leu	Phe	Ala
1				5					10					15	
Ala	Gly	Ser	Thr	Gly	Leu	Thr	Ala	Ala	Ile	Asn	Gln	Met	Thr	Lys	Thr
			20					25					30		
Thr	Ile	Ala	Glu	Gln	Ala	Ser	Leu	Gln	Gln	Lys	Ala	Leu	Phe	Asp	Gln
		35					40					45			
Val	Leu	Pro	Ala	Glu	Arg	Tyr	Asn	Asn	Ala	Leu	Ala	Gln	Ser	Cys	Tyr
	50					55					60				
Leu	Val	Thr	Ala	Pro	Glu	Leu	Gly	Lys	Gly	Glu	His	Arg	Val	Tyr	Ile
65					70					75					80
Ala	Lys	Gln	Asp	Asp	Lys	Pro	Val	Ala	Ala	Val	Leu	Glu	Ala	Thr	Ala
			85						90					95	
Pro	Asp	Gly	Tyr	Ser	Gly	Ala	Ile	Gln	Leu	Leu	Val	Gly	Ala	Asp	Phe
			100					105						110	
Asn	Gly	Thr	Val	Leu	Gly	Thr	Arg	Val	Thr	Glu	His	His	Glu	Thr	Pro
			115				120					125			
Gly	Leu	Gly	Asp	Lys	Ile	Glu	Leu	Arg	Leu	Ser	Asp	Trp	Ile	Thr	His
	130					135					140				
Phe	Ala	Gly	Lys	Lys	Ile	Ser	Gly	Ala	Asp	Asp	Ala	His	Trp	Ala	Val
145					150					155					160
Lys	Lys	Asp	Gly	Gly	Asp	Phe	Asp	Gln	Phe	Thr	Gly	Ala	Thr	Ile	Thr
			165					170						175	
Pro	Arg	Ala	Val	Val	Asn	Ala	Val	Lys	Arg	Ala	Gly	Leu	Tyr	Ala	Gln
			180					185					190		
Thr	Leu	Pro	Ala	Gln	Leu	Ser	Gln	Leu	Pro	Ala	Cys	Gly	Glu		
			195				200					205			

<210> 295
 <211> 231
 <212> PRT
 <213> E. Coli

<400> 295															
Met	Ser	Glu	Ile	Lys	Asp	Val	Ile	Val	Gln	Gly	Leu	Trp	Lys	Asn	Asn
1				5					10					15	
Ser	Ala	Leu	Val	Gln	Leu	Leu	Gly	Leu	Cys	Pro	Leu	Leu	Ala	Val	Thr
			20					25					30		
Ser	Thr	Ala	Thr	Asn	Ala	Leu	Gly	Leu	Gly	Leu	Ala	Thr	Thr	Leu	Val
		35					40					45			
Leu	Thr	Leu	Thr	Asn	Leu	Thr	Ile	Ser	Thr	Leu	Arg	His	Trp	Thr	Pro
	50					55					60				
Ala	Glu	Ile	Arg	Ile	Pro	Ile	Tyr	Val	Met	Ile	Ile	Ala	Ser	Val	Val
65					70					75					80
Ser	Ala	Val	Gln	Met	Leu	Ile	Asn	Ala	Tyr	Ala	Phe	Gly	Leu	Tyr	Gln

				85					90					95			
Ser	Leu	Gly	Ile	Phe	Ile	Pro	Leu	Ile	Val	Thr	Asn	Cys	Ile	Val	Val		
			100						105				110				
Gly	Arg	Ala	Glu	Ala	Phe	Ala	Ala	Lys	Lys	Gly	Pro	Ala	Leu	Ser	Ala		
		115						120				125					
Leu	Asp	Gly	Phe	Ser	Ile	Gly	Met	Gly	Ala	Thr	Cys	Ala	Met	Phe	Val		
	130					135					140						
Leu	Gly	Ser	Leu	Arg	Glu	Ile	Ile	Gly	Asn	Gly	Thr	Leu	Phe	Asp	Gly		
145					150					155					160		
Ala	Asp	Ala	Leu	Leu	Gly	Ser	Trp	Ala	Lys	Val	Leu	Arg	Val	Glu	Ile		
				165					170					175			
Phe	His	Thr	Asp	Ser	Pro	Phe	Leu	Leu	Ala	Met	Leu	Pro	Pro	Gly	Ala		
			180					185				190					
Phe	Ile	Gly	Leu	Gly	Leu	Met	Leu	Ala	Gly	Lys	Tyr	Leu	Ile	Asp	Glu		
	195					200					205						
Arg	Met	Lys	Lys	Arg	Arg	Ala	Glu	Ala	Ala	Ala	Glu	Arg	Ala	Leu	Pro		
	210					215					220						
Asn	Gly	Glu	Thr	Gly	Asn	Val											
225					230												

<210> 296
 <211> 211
 <212> PRT
 <213> E. Coli

<400> 296

Met	Asn	Lys	Ala	Lys	Arg	Leu	Glu	Ile	Leu	Thr	Arg	Leu	Arg	Glu	Asn		
1				5					10					15			
Asn	Pro	His	Pro	Thr	Thr	Glu	Leu	Asn	Phe	Ser	Ser	Pro	Phe	Glu	Leu		
			20					25				30					
Leu	Ile	Ala	Val	Leu	Leu	Ser	Ala	Gln	Ala	Thr	Asp	Val	Ser	Val	Asn		
		35					40				45						
Lys	Ala	Thr	Ala	Lys	Leu	Tyr	Pro	Val	Ala	Asn	Thr	Pro	Ala	Ala	Met		
	50					55					60						
Leu	Glu	Leu	Gly	Val	Glu	Gly	Val	Lys	Thr	Tyr	Ile	Lys	Thr	Ile	Gly		
65					70					75				80			
Leu	Tyr	Asn	Ser	Lys	Ala	Glu	Asn	Ile	Ile	Lys	Thr	Cys	Arg	Ile	Leu		
				85				90						95			
Leu	Glu	Gln	His	Asn	Gly	Glu	Val	Pro	Glu	Asp	Arg	Ala	Ala	Leu	Glu		
		100						105				110					
Ala	Leu	Pro	Gly	Val	Gly	Arg	Lys	Thr	Ala	Asn	Val	Val	Leu	Asn	Thr		
		115					120					125					
Ala	Phe	Gly	Trp	Pro	Thr	Ile	Ala	Val	Asp	Thr	His	Ile	Phe	Arg	Val		
	130					135					140						
Cys	Asn	Arg	Thr	Gln	Phe	Ala	Pro	Gly	Lys	Asn	Val	Glu	Gln	Val	Glu		
145				150						155					160		
Glu	Lys	Leu	Leu	Lys	Val	Val	Pro	Ala	Glu	Phe	Lys	Val	Asp	Cys	His		
				165					170					175			
His	Trp	Leu	Ile	Leu	His	Gly	Arg	Tyr	Thr	Cys	Ile	Ala	Arg	Lys	Pro		
		180				185					190						
Arg	Cys	Gly	Ser	Cys	Ile	Ile	Glu	Asp	Leu	Cys	Glu	Tyr	Lys	Glu	Lys		
	195					200					205						
Val	Asp	Ile															
	210																

<210> 297
 <211> 167
 <212> PRT
 <213> E. Coli

<400> 297

Met	Lys	Arg	Leu	His	Lys	Arg	Phe	Leu	Leu	Ala	Thr	Phe	Cys	Ala	Leu
1				5					10					15	
Phe	Thr	Ala	Thr	Leu	Gln	Ala	Ala	Asp	Val	Thr	Ile	Thr	Val	Asn	Gly
			20					25					30		
Arg	Val	Val	Ala	Lys	Pro	Cys	Thr	Ile	Gln	Thr	Lys	Glu	Ala	Asn	Val
		35					40					45			
Asn	Leu	Gly	Asp	Leu	Tyr	Thr	Arg	Asn	Leu	Gln	Gln	Pro	Gly	Ser	Ala
	50					55					60				
Ser	Gly	Trp	His	Asn	Ile	Thr	Leu	Ser	Leu	Thr	Asp	Cys	Pro	Val	Glu
65				70						75				80	
Thr	Ser	Ala	Val	Thr	Ala	Ile	Val	Thr	Gly	Ser	Thr	Asp	Asn	Thr	Gly
			85						90					95	
Tyr	Tyr	Lys	Asn	Glu	Gly	Thr	Ala	Glu	Asn	Ile	Gln	Ile	Glu	Leu	Arg
			100					105					110		
Asp	Asp	Gln	Asp	Ala	Ala	Leu	Lys	Asn	Gly	Asp	Ser	Lys	Thr	Val	Ile
		115					120					125			
Val	Asp	Glu	Ile	Thr	Arg	Asn	Ala	Gln	Phe	Pro	Leu	Lys	Ala	Arg	Ala
	130					135					140				
Ile	Thr	Val	Asn	Gly	Asn	Ala	Ser	Gln	Gly	Thr	Ile	Glu	Ala	Leu	Ile
145					150					155					160
Asn	Val	Ile	Tyr	Thr	Trp	Gln									
				165											

<210> 298
 <211> 176
 <212> PRT
 <213> E. Coli

<400> 298

Met	Lys	Tyr	Asn	Asn	Ile	Ile	Phe	Leu	Gly	Leu	Cys	Leu	Gly	Leu	Thr
1				5					10					15	
Thr	Tyr	Ser	Ala	Leu	Ser	Ala	Asp	Ser	Val	Ile	Lys	Ile	Ser	Gly	Arg
			20					25					30		
Val	Leu	Asp	Tyr	Gly	Cys	Thr	Val	Ser	Ser	Asp	Ser	Leu	Asn	Phe	Thr
		35					40					45			
Val	Asp	Leu	Gln	Lys	Asn	Ser	Ala	Arg	Gln	Phe	Pro	Thr	Thr	Gly	Ser
	50					55					60				
Thr	Ser	Pro	Ala	Val	Pro	Phe	Gln	Ile	Thr	Leu	Ser	Glu	Cys	Ser	Lys
65				70						75				80	
Gly	Thr	Thr	Gly	Val	Arg	Val	Ala	Phe	Asn	Gly	Ile	Glu	Asp	Ala	Glu
			85						90					95	
Asn	Asn	Thr	Leu	Leu	Lys	Leu	Asp	Glu	Gly	Ser	Asn	Thr	Ala	Ser	Gly
			100					105					110		
Leu	Gly	Ile	Glu	Ile	Leu	Asp	Ala	Asn	Met	Arg	Pro	Val	Lys	Leu	Asn
		115				120						125			
Asp	Leu	His	Ala	Gly	Met	Gln	Trp	Ile	Pro	Leu	Val	Pro	Glu	Gln	Asn
	130					135					140				
Asn	Ile	Leu	Pro	Tyr	Ser	Ala	Arg	Leu	Lys	Ser	Thr	Gln	Lys	Ser	Val
145					150					155					160

Asn	Pro	Gly	Leu	Val	Arg	Ala	Ser	Ala	Thr	Phe	Thr	Leu	Glu	Phe	Gln
				165					170					175	

<210> 299
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 <212> PRT
 <213> E. Coli

<400> 299

Met	Ser	Gly	Tyr	Thr	Val	Lys	Pro	Pro	Thr	Gly	Asp	Thr	Asn	Glu	Gln
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Thr	Gln	Phe	Ile	Asp	Tyr	Phe	Asn	Leu	Phe	Tyr	Ser	Lys	Arg	Gly	Gln
			20					25					30		
Glu	Gln	Ile	Ser	Ile	Ser	Gln	Gln	Leu	Gly	Asn	Tyr	Gly	Thr	Thr	Phe
		35					40					45			
Phe	Ser	Ala	Ser	Arg	Gln	Ser	Tyr	Trp	Asn	Thr	Ser	Arg	Ser	Asp	Gln
	50					55					60				
Gln	Ile	Ser	Phe	Gly	Leu	Asn	Val	Pro	Phe	Gly	Asp	Ile	Thr	Thr	Ser
65				70						75					80
Leu	Asn	Tyr	Ser	Tyr	Ser	Asn	Asn	Ile	Trp	Gln	Asn	Asp	Arg	Asp	His
			85						90					95	
Leu	Leu	Ala	Phe	Thr	Leu	Asn	Val	Pro	Phe	Ser	His	Trp	Met	Arg	Thr
		100						105					110		
Asp	Ser	Gln	Ser	Ala	Phe	Arg	Asn	Ser	Asn	Ala	Ser	Tyr	Ser	Met	Ser
		115					120					125			
Asn	Asp	Leu	Lys	Gly	Gly	Met	Thr	Asn	Leu	Ser	Gly	Val	Tyr	Gly	Thr
	130					135					140				
Leu	Leu	Pro	Asp	Asn	Asn	Leu	Asn	Tyr	Ser	Val	Gln	Val	Gly	Asn	Thr
145				150						155					160
His	Gly	Gly	Asn	Thr	Ser	Ser	Gly	Thr	Ser	Gly	Tyr	Ser	Ser	Leu	Asn
			165					170						175	
Tyr	Arg	Gly	Ala	Tyr	Gly	Asn	Thr	Asn	Val	Gly	Tyr	Ser	Arg	Ser	Gly
		180					185						190		
Asp	Ser	Ser	Gln	Ile	Tyr	Tyr	Gly	Met	Ser	Gly	Gly	Ile	Ile	Ala	His
		195					200					205			
Ala	Asp	Gly	Ile	Thr	Phe	Gly	Gln	Pro	Leu	Gly	Asp	Thr	Met	Val	Leu
	210					215					220				
Val	Lys	Ala	Pro	Gly	Ala	Asp	Asn	Val	Lys	Ile	Glu	Asn	Gln	Thr	Gly
225				230						235					240
Ile	His	Thr	Asp	Trp	Arg	Gly	Tyr	Ala	Ile	Leu	Pro	Phe	Ala	Thr	Glu
			245						250					255	
Tyr	Arg	Glu	Asn	Arg	Val	Ala	Leu	Asn	Ala	Asn	Ser	Leu	Ala	Asp	Asn
		260						265					270		
Val	Glu	Leu	Asp	Glu	Thr	Val	Val	Thr	Val	Ile	Pro	Thr	His	Gly	Ala
	275						280					285			
Ile	Ala	Arg	Ala	Thr	Phe	Asn	Ala	Gln	Ile	Gly	Gly	Lys	Val	Leu	Met
	290					295					300				
Thr	Leu	Lys	Tyr	Gly	Asn	Lys	Ser	Val	Pro	Phe	Gly	Ala	Ile	Val	Thr
305				310						315					320
His	Gly	Glu	Asn	Lys	Asn	Gly	Ser	Ile	Val	Ala	Glu	Asn	Gly	Gln	Val
			325						330					335	
Tyr	Leu	Thr	Gly	Leu	Pro	Gln	Ser	Gly	Gln	Leu	Gln	Val	Ser	Trp	Gly
		340						345					350		
Lys	Asp	Lys	Asn	Ser	Asn	Cys	Ile	Val	Glu	Tyr	Lys	Leu	Pro	Glu	Val
		355					360					365			

Ser Pro Gly Thr Leu Leu Asn Gln Gln Thr Ala Ile Cys Arg
 370 375 380

<210> 300
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 <212> PRT
 <213> E. Coli

<400> 300

Met Ile Ala Ile Ala Asp Ile Leu Gln Ala Gly Glu Lys Leu Thr Ala
 1 5 10 15
 Val Ala Pro Phe Leu Ala Gly Ile Gln Asn Glu Glu Gln Tyr Thr Gln
 20 25 30
 Ala Leu Glu Leu Val Asp His Leu Leu Leu Asn Asp Pro Glu Asn Pro
 35 40 45
 Leu Leu Asp Leu Val Cys Ala Lys Ile Thr Ala Trp Glu Glu Ser Ala
 50 55 60
 Pro Glu Phe Ala Glu Phe Asn Ala Met Ala Gln Ala Met Pro Gly Gly
 65 70 75 80
 Ile Ala Val Ile Arg Thr Leu Met Asp Gln Tyr Gly Leu Thr Leu Ser
 85 90 95
 Asp Leu Pro Glu Ile Gly Ser Lys Ser Met Val Ser Arg Val Leu Ser
 100 105 110
 Gly Lys Arg Lys Leu Thr Leu Glu His Ala Lys Lys Leu Ala Thr Arg
 115 120 125
 Phe Gly Ile Ser Pro Ala Leu Phe Ile Asp
 130 135

<210> 301
 <211> 104
 <212> PRT
 <213> E. Coli

<400> 301

Met His Leu Ile Thr Gln Lys Ala Leu Lys Asp Ala Ala Glu Lys Tyr
 1 5 10 15
 Pro Gln His Lys Thr Glu Leu Val Ala Leu Gly Asn Thr Ile Ala Lys
 20 25 30
 Gly Tyr Phe Lys Lys Pro Glu Ser Leu Lys Ala Val Phe Pro Ser Leu
 35 40 45
 Asp Asn Phe Lys Tyr Leu Asp Lys His Tyr Val Phe Asn Val Gly Gly
 50 55 60
 Asn Glu Leu Arg Val Val Ala Met Val Phe Phe Glu Ser Gln Lys Cys
 65 70 75 80
 Tyr Ile Arg Glu Val Met Thr His Lys Glu Tyr Asp Phe Phe Thr Ala
 85 90 95
 Val His Arg Thr Lys Gly Lys Lys
 100

<210> 302
 <211> 2383
 <212> PRT
 <213> E. Coli

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<400> 302
Met Leu Ser Val Phe Thr Phe Phe Arg Cys Ala Arg Lys Gly Ala Phe
1      5      10      15
Met Leu Ala Arg Ser Gly Lys Val Ser Met Ala Thr Lys Lys Arg Ser
20     25     30
Gly Glu Glu Ile Asn Asp Arg Gln Ile Leu Cys Gly Met Gly Ile Lys
35     40     45
Leu Arg Arg Leu Thr Ala Gly Ile Cys Leu Ile Thr Gln Leu Ala Phe
50     55     60
Pro Met Ala Ala Ala Ala Gln Gly Val Val Asn Ala Ala Thr Gln Gln
65     70     75     80
Pro Val Pro Ala Gln Ile Ala Ile Ala Asn Ala Asn Thr Val Pro Tyr
85     90     95
Thr Leu Gly Ala Leu Glu Ser Ala Gln Ser Val Ala Glu Arg Phe Gly
100    105    110
Ile Ser Val Ala Glu Leu Arg Lys Leu Asn Gln Phe Arg Thr Phe Ala
115    120    125
Arg Ser Phe Asp Asn Val Arg Gln Gly Asp Glu Leu Asp Val Pro Ala
130    135    140
Gln Val Ser Glu Lys Lys Leu Thr Pro Pro Pro Gly Asn Ser Ser Asp
145    150    155    160
Asn Leu Glu Gln Gln Ile Ala Ser Thr Ser Gln Gln Ile Gly Ser Leu
165    170    175
Leu Ala Glu Asp Met Asn Ser Glu Gln Ala Ala Asn Met Ala Arg Gly
180    185    190
Trp Ala Ser Ser Gln Ala Ser Gly Ala Met Thr Asp Trp Leu Ser Arg
195    200    205
Phe Gly Thr Ala Arg Ile Thr Leu Gly Val Asp Glu Asp Phe Ser Leu
210    215    220
Lys Asn Ser Gln Phe Asp Phe Leu His Pro Trp Tyr Glu Thr Pro Asp
225    230    235    240
Asn Leu Phe Phe Ser Gln His Thr Leu His Arg Thr Asp Glu Arg Thr
245    250    255
Gln Ile Asn Asn Gly Leu Gly Trp Arg His Phe Thr Pro Thr Trp Met
260    265    270
Ser Gly Ile Asn Phe Phe Phe Asp His Asp Leu Ser Arg Tyr His Ser
275    280    285
Arg Ala Gly Ile Gly Ala Glu Tyr Trp Arg Asp Tyr Leu Lys Leu Ser
290    295    300
Ser Asn Gly Tyr Leu Arg Leu Thr Asn Trp Arg Ser Ala Pro Glu Leu
305    310    315    320
Asp Asn Asp Tyr Glu Ala Arg Pro Ala Asn Gly Trp Asp Val Arg Ala
325    330    335
Glu Ser Trp Leu Pro Ala Trp Pro His Leu Gly Gly Lys Leu Val Tyr
340    345    350
Glu Gln Tyr Tyr Gly Asp Glu Val Ala Leu Phe Asp Lys Asp Asp Arg
355    360    365
Gln Ser Asn Pro His Ala Ile Thr Ala Gly Leu Asn Tyr Thr Pro Phe
370    375    380
Pro Leu Met Thr Phe Ser Ala Glu Gln Arg Gln Gly Lys Gln Gly Glu
385    390    395    400
Asn Asp Thr Arg Phe Ala Val Asp Phe Thr Trp Gln Pro Gly Ser Ala
405    410    415
Met Gln Lys Gln Leu Asp Pro Asn Glu Val Ala Ala Arg Arg Ser Leu
420    425    430
Ala Gly Ser Arg Tyr Asp Leu Val Asp Arg Asn Asn Asn Ile Val Leu

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		435				440				445					
Glu	Tyr	Arg	Lys	Lys	Glu	Leu	Val	Arg	Leu	Thr	Leu	Thr	Asp	Pro	Val
	450					455					460				
Thr	Gly	Lys	Ser	Gly	Glu	Val	Lys	Ser	Leu	Val	Ser	Ser	Leu	Gln	Thr
465					470					475					480
Lys	Tyr	Ala	Leu	Lys	Gly	Tyr	Asn	Val	Glu	Ala	Thr	Ala	Leu	Glu	Ala
				485					490					495	
Ala	Gly	Gly	Lys	Val	Val	Thr	Thr	Gly	Lys	Asp	Ile	Leu	Val	Thr	Leu
			500					505					510		
Pro	Ala	Tyr	Arg	Phe	Thr	Ser	Thr	Pro	Glu	Thr	Asp	Asn	Thr	Trp	Pro
		515					520					525			
Ile	Glu	Val	Thr	Ala	Glu	Asp	Val	Lys	Gly	Asn	Leu	Ser	Asn	Arg	Glu
	530					535					540				
Gln	Ser	Met	Val	Val	Val	Gln	Ala	Pro	Thr	Leu	Ser	Gln	Lys	Asp	Ser
545					550					555					560
Ser	Val	Ser	Leu	Ser	Thr	Gln	Thr	Leu	Asn	Ala	Asp	Ser	His	Ser	Thr
				565					570					575	
Ala	Thr	Leu	Thr	Phe	Ile	Ala	His	Asp	Ala	Ala	Gly	Asn	Pro	Val	Val
			580					585					590		
Gly	Leu	Val	Leu	Ser	Thr	Arg	His	Glu	Gly	Val	Gln	Asp	Ile	Thr	Leu
	595					600					605				
Ser	Asp	Trp	Lys	Asp	Asn	Gly	Asp	Gly	Ser	Tyr	Thr	Gln	Ile	Leu	Thr
	610					615					620				
Thr	Gly	Ala	Met	Ser	Gly	Thr	Leu	Thr	Leu	Met	Pro	Gln	Leu	Asn	Gly
625					630					635					640
Val	Asp	Ala	Ala	Lys	Ala	Pro	Ala	Val	Val	Asn	Ile	Ile	Ser	Val	Ser
				645					650					655	
Ser	Ser	Arg	Thr	His	Ser	Ser	Ile	Lys	Ile	Asp	Lys	Asp	Arg	Tyr	Leu
		660						665					670		
Ser	Gly	Asn	Pro	Ile	Glu	Val	Thr	Val	Glu	Leu	Arg	Asp	Glu	Asn	Asp
	675						680					685			
Lys	Pro	Val	Lys	Glu	Gln	Lys	Gln	Gln	Leu	Asn	Asn	Ala	Val	Ser	Ile
	690					695					700				
Asp	Asn	Val	Lys	Pro	Gly	Val	Thr	Thr	Asp	Trp	Lys	Glu	Thr	Ala	Asp
705					710				715						720
Gly	Val	Tyr	Lys	Ala	Thr	Tyr	Thr	Ala	Tyr	Thr	Lys	Gly	Ser	Gly	Leu
			725					730					735		
Thr	Ala	Lys	Leu	Leu	Met	Gln	Asn	Trp	Asn	Glu	Asp	Leu	His	Thr	Ala
		740					745					750			
Gly	Phe	Ile	Ile	Asp	Ala	Asn	Pro	Gln	Ser	Ala	Lys	Ile	Ala	Thr	Leu
	755					760					765				
Ser	Ala	Ser	Asn	Asn	Gly	Val	Leu	Ala	Asn	Glu	Asn	Ala	Ala	Asn	Thr
	770				775					780					
Val	Ser	Val	Asn	Val	Ala	Asp	Glu	Gly	Ser	Asn	Pro	Ile	Asn	Asp	His
785				790					795						800
Thr	Val	Thr	Phe	Ala	Val	Leu	Ser	Gly	Ser	Ala	Thr	Ser	Phe	Asn	Asn
			805					810					815		
Gln	Asn	Thr	Ala	Lys	Thr	Asp	Val	Asn	Gly	Leu	Ala	Thr	Phe	Asp	Leu
		820					825					830			
Lys	Ser	Ser	Lys	Gln	Glu	Asp	Asn	Thr	Val	Glu	Val	Thr	Leu	Glu	Asn
	835					840					845				
Gly	Val	Lys	Gln	Thr	Leu	Ile	Val	Ser	Phe	Val	Gly	Asp	Ser	Ser	Thr
	850				855				860						
Ala	Gln	Val	Asp	Leu	Gln	Lys	Ser	Lys	Asn	Glu	Val	Val	Ala	Asp	Gly
865				870					875						880
Asn	Asp	Ser	Val	Thr	Met	Thr	Ala	Thr	Val	Arg	Asp	Ala	Lys	Gly	Asn
			885					890						895	

Lys Ala His Val Asn Asp Gln Phe Gly Asn Pro Val Ala His Gln Pro
 1810 1815 1820
 Val Thr Phe Ser Ala Glu Pro Ser Ser Gln Met Ile Ile Ser Gln Asn
 1825 1830 1835 1840
 Thr Val Ser Thr Asn Thr Gln Gly Val Ala Glu Val Thr Met Thr Pro
 1845 1850 1855
 Glu Arg Asn Gly Ser Tyr Met Val Lys Ala Ser Leu Pro Asn Gly Ala
 1860 1865 1870
 Ser Leu Glu Lys Gln Leu Glu Ala Ile Asp Glu Lys Leu Thr Leu Thr
 1875 1880 1885
 Ala Ser Ser Pro Leu Ile Gly Val Tyr Ala Pro Thr Gly Ala Thr Leu
 1890 1895 1900
 Thr Ala Thr Leu Thr Ser Ala Asn Gly Thr Pro Val Glu Gly Gln Val
 1905 1910 1915 1920
 Ile Asn Phe Ser Val Thr Pro Glu Gly Ala Thr Leu Ser Gly Gly Lys
 1925 1930 1935
 Val Arg Thr Asn Ser Ser Gly Gln Ala Pro Val Val Leu Thr Ser Asn
 1940 1945 1950
 Lys Val Gly Thr Tyr Thr Val Thr Ala Ser Phe His Asn Gly Val Thr
 1955 1960 1965
 Ile Gln Thr Gln Thr Thr Val Lys Val Thr Gly Asn Ser Ser Thr Ala
 1970 1975 1980
 His Val Ala Ser Phe Ile Ala Asp Pro Ser Thr Ile Ala Ala Thr Asn
 1985 1990 1995 2000
 Thr Asp Leu Ser Thr Leu Lys Ala Thr Val Glu Asp Gly Ser Gly Asn
 2005 2010 2015
 Leu Ile Glu Gly Leu Thr Val Tyr Phe Ala Leu Lys Ser Gly Ser Ala
 2020 2025 2030
 Thr Leu Thr Ser Leu Thr Ala Val Thr Asp Gln Asn Gly Ile Ala Thr
 2035 2040 2045
 Thr Ser Val Lys Gly Ala Met Thr Gly Ser Val Thr Val Ser Ala Val
 2050 2055 2060
 Thr Thr Ala Gly Gly Met Gln Thr Val Asp Ile Thr Leu Val Ala Gly
 2065 2070 2075 2080
 Pro Ala Asp Thr Ser Gln Ser Val Leu Lys Ser Asn Arg Ser Ser Leu
 2085 2090 2095
 Lys Gly Asp Tyr Thr Asp Ser Ala Glu Leu Arg Leu Val Leu His Asp
 2100 2105 2110
 Ile Ser Gly Asn Pro Ile Lys Val Ser Glu Gly Met Glu Phe Val Gln
 2115 2120 2125
 Ser Gly Thr Asn Val Pro Tyr Ile Lys Ile Ser Ala Ile Asp Tyr Ser
 2130 2135 2140
 Leu Asn Ile Asn Gly Asp Tyr Lys Ala Thr Val Thr Gly Gly Gly Glu
 2145 2150 2155 2160
 Gly Ile Ala Thr Leu Ile Pro Val Leu Asn Gly Val His Gln Ala Gly
 2165 2170 2175
 Leu Ser Thr Thr Ile Gln Phe Thr Arg Ala Glu Asp Lys Ile Met Ser
 2180 2185 2190
 Gly Thr Val Ser Val Asn Gly Thr Asp Leu Pro Thr Thr Thr Phe Pro
 2195 2200 2205
 Ser Gln Gly Phe Thr Gly Ala Tyr Tyr Gln Leu Asn Asn Asp Asn Phe
 2210 2215 2220
 Ala Pro Gly Lys Thr Ala Ala Asp Tyr Glu Phe Ser Ser Ser Ala Ser
 2225 2230 2235 2240
 Trp Val Asp Val Asp Ala Thr Gly Lys Val Thr Phe Lys Asn Val Gly
 2245 2250 2255
 Ser Asn Ser Glu Arg Ile Thr Ala Thr Pro Lys Ser Gly Gly Pro Ser

	2260		2265		2270
Tyr Val	Tyr Glu Ile Arg Val	Lys Ser Trp Trp Val	Asn Ala Gly Glu		
	2275	2280	2285		
Ala Phe Met	Ile Tyr Ser Leu Ala Glu Asn Phe	Cys Ser Ser Asn Gly			
	2290	2295	2300		
Tyr Thr Leu	Pro Arg Ala Asn Tyr Leu Asn His	Cys Ser Ser Arg Gly			
2305	2310	2315	2320		
Ile Gly Ser	Leu Tyr Ser Glu Trp Gly Asp Met Gly	His Tyr Thr Thr			
	2325	2330	2335		
Asp Ala Gly	Phe Gln Ser Asn Met Tyr Trp Ser Ser	Pro Ala Asn			
	2340	2345	2350		
Ser Ser Glu	Gln Tyr Val Val Ser Leu Ala Thr Gly	Asp Gln Ser Val			
	2355	2360	2365		
Phe Glu Lys	Leu Gly Phe Ala Tyr Ala Thr Cys Tyr	Lys Asn Leu			
2370	2375	2380			

<210> 303
 <211> 61
 <212> PRT
 <213> E. Coli

<400> 303														
Met Ser Lys	Gly Ala Leu Tyr Glu Phe Asn Asn Pro Asp Gln Leu Lys													
1	5 10 15													
Ile Pro Leu	Pro His Lys His Ile Ala Ser Thr Phe Asn Asp Ile Met													
	20 25 30													
Ser Lys Asp	Val Gly Tyr Ala Tyr Val Ser Leu Leu Tyr Ala Cys Pro													
	35 40 45													
Leu Lys Thr	His Ser Leu Arg Leu Asn Pro Phe Ser Lys													
50	55 60													

<210> 304
 <211> 398
 <212> PRT
 <213> E. Coli

<400> 304														
Met Gln Val	Ala Glu Gln Arg Ile Gln Leu Ala Glu Ala Gln Ala Lys													
1	5 10 15													
Ala Val Ala	Thr Gln Asp Gly Pro Gln Ile Asp Phe Ser Ala Asp Met													
	20 25 30													
Glu Arg Gln	Lys Met Ser Ala Glu Gly Leu Met Gly Pro Phe Ala Leu													
	35 40 45													
Asn Asp Pro	Ala Ala Gly Thr Gly Pro Trp Tyr Thr Asn Gly Thr													
50	55 60													
Phe Gly Leu	Thr Ala Gly Trp His Leu Asp Ile Trp Gly Lys Asn Arg													
65	70 75 80													
Ala Glu Val	Thr Ala Arg Leu Gly Thr Val Lys Ala Arg Ala Ala Glu													
	85 90 95													
Arg Glu Gln	Thr Arg Gln Leu Leu Ala Gly Ser Val Ala Arg Leu Tyr													
	100 105 110													
Trp Glu Trp	Gln Thr Gln Ala Ala Leu Asn Thr Val Leu Gln Gln Ile													
	115 120 125													
Glu Lys Glu	Gln Asn Thr Ile Ile Ala Thr Asp Arg Gln Leu Tyr Gln													
130	135 140													

Asn	Gly	Ile	Thr	Ser	Ser	Val	Glu	Gly	Val	Glu	Thr	Asp	Ile	Asn	Ala
145					150					155					160
Ser	Lys	Thr	Arg	Gln	Gln	Leu	Asn	Asp	Val	Ala	Gly	Lys	Met	Lys	Ile
				165					170						175
Ile	Glu	Ala	Arg	Leu	Ser	Ala	Leu	Thr	Asn	Asn	Gln	Thr	Lys	Ser	Leu
			180					185					190		
Lys	Leu	Lys	Pro	Val	Ala	Leu	Pro	Lys	Val	Ala	Ser	Gln	Leu	Pro	Asp
		195					200					205			
Glu	Leu	Gly	Tyr	Ser	Leu	Leu	Ala	Arg	Arg	Ala	Asp	Leu	Gln	Ala	Ala
	210					215					220				
His	Trp	Tyr	Val	Glu	Ser	Ser	Leu	Ser	Thr	Ile	Asp	Ala	Ala	Lys	Ala
225					230					235					240
Ala	Phe	Tyr	Pro	Asp	Ile	Asn	Leu	Met	Ala	Phe	Leu	Gln	Gln	Asp	Ala
				245					250					255	
Leu	His	Leu	Ser	Asp	Leu	Phe	Arg	His	Ser	Ala	Gln	Gln	Met	Gly	Val
			260					265					270		
Thr	Ala	Gly	Leu	Thr	Leu	Pro	Ile	Phe	Asp	Ser	Gly	Arg	Leu	Asn	Ala
		275					280					285			
Asn	Leu	Asp	Ile	Ala	Lys	Ala	Glu	Ser	Asn	Leu	Ser	Ile	Ala	Ser	Tyr
	290					295					300				
Asn	Lys	Ala	Val	Val	Glu	Ala	Val	Asn	Asp	Val	Ala	Arg	Ala	Ala	Ser
305					310					315					320
Gln	Val	Gln	Thr	Leu	Ala	Glu	Lys	Asn	Gln	His	Gln	Ala	Gln	Ile	Glu
				325					330					335	
Arg	Asp	Ala	Leu	Arg	Val	Val	Gly	Leu	Ala	Gln	Ala	Arg	Phe	Asn	Ala
			340					345					350		
Gly	Ile	Ile	Ala	Gly	Ser	Arg	Val	Ser	Glu	Ala	Arg	Ile	Pro	Ala	Leu
		355					360					365			
Arg	Glu	Arg	Ala	Asn	Gly	Leu	Leu	Gln	Gly	Gln	Trp	Leu	Asp	Ala	
	370					375				380					
Ser	Ile	Gln	Leu	Thr	Gly	Ala	Leu	Gly	Gly	Gly	Tyr	Lys	Arg		
385					390					395					

<210> 305
 <211> 96
 <212> PRT
 <213> E. Coli

<400> 305															
Met	Tyr	Cys	His	Ala	Lys	Leu	Lys	Asn	Ile	Ser	Gln	His	Thr	Val	Ile
1				5					10					15	
Ser	Ala	His	Leu	Phe	Leu	Pro	Asp	Tyr	Ser	Pro	Met	Asn	Arg	Asp	Ser
			20					25					30		
Phe	Tyr	Pro	Ala	Ile	Ala	Cys	Phe	Pro	Leu	Leu	Leu	Met	Leu	Ala	Gly
		35					40					45			
Cys	Ala	Pro	Met	His	Glu	Thr	Arg	Gln	Ala	Leu	Ser	Gln	Gln	Thr	Pro
		50				55					60				
Ala	Ala	Gln	Val	Asp	Thr	Ala	Leu	Pro	Thr	Ala	Leu	Lys	Met	Val	Gly
65					70					75					80
Gln	Thr	Ala	Asn	Gly	Gly	Trp	Ser	Ile	Thr	Ile	Ile	Asn	Ser	Leu	Pro
				85					90					95	

<210> 306
 <211> 315
 <212> PRT

<213> E. Coli

<400> 306

Met Arg Val Leu Leu Ala Pro Met Glu Gly Val Leu Asp Ser Leu Val
1 5 10 15
Arg Glu Leu Leu Thr Glu Val Asn Asp Tyr Asp Leu Cys Ile Thr Glu
20 25 30
Phe Val Arg Val Val Asp Gln Leu Pro Val Lys Val Phe His Arg
35 40 45
Ile Cys Pro Glu Leu Gln Asn Ala Ser Arg Thr Pro Ser Gly Thr Leu
50 55 60
Val Arg Val Gln Leu Leu Gly Gln Phe Pro Gln Trp Leu Ala Glu Asn
65 70 75 80
Ala Ala Arg Ala Val Glu Leu Gly Ser Trp Gly Val Asp Leu Asn Cys
85 90 95
Gly Cys Pro Ser Lys Thr Val Asn Gly Ser Gly Gly Gly Ala Thr Leu
100 105 110
Leu Lys Asp Pro Glu Leu Ile Tyr Gln Gly Ala Lys Ala Met Arg Glu
115 120 125
Ala Val Pro Ala His Leu Pro Val Ser Val Lys Val Arg Leu Gly Trp
130 135 140
Asp Ser Gly Glu Lys Lys Phe Glu Ile Ala Asp Ala Val Gln Gln Ala
145 150 155 160
Gly Ala Thr Glu Leu Val Val His Gly Arg Thr Lys Glu Gln Gly Tyr
165 170 175
Arg Ala Glu His Ile Asp Trp Gln Ala Ile Gly Asp Ile Arg Gln Arg
180 185 190
Leu Asn Ile Pro Val Ile Ala Asn Gly Glu Ile Trp Asp Trp Gln Ser
195 200 205
Ala Gln Gln Cys Met Ala Ile Ser Gly Cys Asp Ala Val Met Ile Gly
210 215 220
Arg Gly Ala Leu Asn Ile Pro Asn Leu Ser Arg Val Val Lys Tyr Asn
225 230 235 240
Glu Pro Arg Met Pro Trp Pro Glu Val Val Ala Leu Leu Gln Lys Tyr
245 250 255
Thr Arg Leu Glu Lys Gln Gly Asp Thr Gly Leu Tyr His Val Ala Arg
260 265 270
Ile Lys Gln Trp Leu Ser Tyr Leu Arg Lys Glu Tyr Asp Glu Ala Thr
275 280 285
Glu Leu Phe Gln His Val Arg Val Leu Asn Asn Ser Pro Asp Ile Ala
290 295 300
Arg Ala Ile Gln Ala Ile Asp Ile Glu Lys Leu
305 310 315

<210> 307

<211> 296

<212> PRT

<213> E. Coli

<400> 307

Met Thr Ile Ser Thr Thr Ser Thr Pro His Asp Ala Val Phe Lys Ser
1 5 10 15
Phe Leu Arg His Pro Asp Thr Ala Arg Asp Phe Ile Asp Ile His Leu
20 25 30
Pro Ala Pro Leu Arg Lys Leu Cys Asp Leu Thr Thr Leu Lys Leu Glu
35 40 45

Pro	Asn	Ser	Phe	Ile	Asp	Glu	Asp	Leu	Arg	Gln	Tyr	Tyr	Ser	Asp	Leu
50						55					60				
Leu	Trp	Ser	Val	Lys	Thr	Gln	Glu	Gly	Val	Gly	Tyr	Ile	Tyr	Val	Val
65					70					75					80
Ile	Glu	His	Gln	Ser	Lys	Pro	Glu	Glu	Leu	Met	Ala	Phe	Arg	Met	Met
			85						90					95	
Arg	Tyr	Ser	Ile	Ala	Ala	Met	Gln	Asn	His	Leu	Asp	Ala	Gly	Tyr	Lys
			100					105					110		
Glu	Leu	Pro	Leu	Val	Leu	Pro	Met	Leu	Phe	Tyr	His	Gly	Cys	Arg	Ser
	115						120					125			
Pro	Tyr	Pro	Tyr	Ser	Leu	Cys	Trp	Leu	Asp	Glu	Phe	Ala	Glu	Pro	Ala
	130					135					140				
Ile	Ala	Arg	Lys	Ile	Tyr	Ser	Ser	Ala	Phe	Pro	Leu	Val	Asp	Ile	Thr
145					150					155					160
Val	Val	Pro	Asp	Asp	Glu	Ile	Met	Gln	His	Arg	Lys	Met	Ala	Leu	Leu
			165					170						175	
Glu	Leu	Ile	Gln	Lys	His	Ile	Arg	Gln	Arg	Asp	Leu	Leu	Gly	Leu	Val
			180					185					190		
Asp	Gln	Ile	Val	Ser	Leu	Leu	Val	Thr	Gly	Asn	Thr	Asn	Asp	Arg	Gln
	195						200					205			
Leu	Lys	Ala	Leu	Phe	Asn	Tyr	Val	Leu	Gln	Thr	Gly	Asp	Ala	Gln	Arg
	210					215					220				
Phe	Arg	Ala	Phe	Ile	Gly	Glu	Ile	Ala	Glu	Arg	Ala	Pro	Gln	Glu	Lys
225					230					235					240
Glu	Lys	Leu	Met	Thr	Ile	Ala	Asp	Arg	Leu	Arg	Glu	Glu	Gly	Ala	Met
			245					250						255	
Gln	Gly	Lys	His	Glu	Glu	Ala	Leu	Arg	Ile	Ala	Gln	Glu	Met	Leu	Asp
		260					265						270		
Arg	Gly	Leu	Asp	Arg	Glu	Leu	Val	Met	Met	Val	Thr	Arg	Leu	Ser	Pro
	275						280					285			
Asp	Asp	Leu	Ile	Ala	Gln	Ser	His								
	290					295									

<210> 308
 <211> 555
 <212> PRT
 <213> E. Coli

<400> 308

Met	Ala	Gln	Phe	Val	Tyr	Thr	Met	His	Arg	Val	Gly	Lys	Val	Val	Pro
1				5					10					15	
Pro	Lys	Arg	His	Ile	Leu	Lys	Asn	Ile	Ser	Leu	Ser	Phe	Phe	Pro	Gly
		20					25						30		
Ala	Lys	Ile	Gly	Val	Leu	Gly	Leu	Asn	Gly	Ala	Gly	Lys	Ser	Thr	Leu
	35						40					45			
Leu	Arg	Ile	Met	Ala	Gly	Ile	Asp	Lys	Asp	Ile	Glu	Gly	Glu	Ala	Arg
	50					55					60				
Pro	Gln	Pro	Asp	Ile	Lys	Ile	Gly	Tyr	Leu	Pro	Gln	Glu	Pro	Gln	Leu
65				70					75						80
Asn	Pro	Glu	His	Thr	Val	Arg	Glu	Ser	Ile	Glu	Glu	Ala	Val	Ser	Glu
			85					90						95	
Val	Val	Asn	Ala	Leu	Lys	Arg	Leu	Asp	Glu	Val	Tyr	Ala	Leu	Tyr	Ala
		100						105					110		
Asp	Pro	Asp	Ala	Asp	Phe	Asp	Lys	Leu	Ala	Ala	Glu	Gln	Gly	Arg	Leu
	115						120					125			
Glu	Glu	Ile	Ile	Gln	Ala	His	Asp	Gly	His	Asn	Leu	Asn	Val	Gln	Leu

<211> 173
 <212> PRT
 <213> E. Coli

<400> 309

Met	Ser	Lys	Pro	Lys	Tyr	Pro	Phe	Glu	Lys	Arg	Leu	Glu	Val	Val	Asn
1				5					10					15	
His	Tyr	Phe	Thr	Thr	Asp	Asp	Gly	Tyr	Arg	Ile	Ile	Ser	Ala	Arg	Phe
			20					25					30		
Gly	Val	Pro	Arg	Thr	Gln	Val	Arg	Thr	Trp	Val	Ala	Leu	Tyr	Glu	Lys
		35					40					45			
His	Gly	Glu	Lys	Gly	Leu	Ile	Pro	Lys	Pro	Lys	Gly	Val	Ser	Ala	Asp
	50					55					60				
Pro	Glu	Leu	Arg	Ile	Lys	Val	Val	Lys	Ala	Val	Ile	Glu	Gln	His	Met
65					70					75					80
Ser	Leu	Asn	Gln	Ala	Ala	Ala	His	Phe	Met	Leu	Ala	Gly	Ser	Gly	Ser
				85					90					95	
Val	Ala	Arg	Trp	Leu	Lys	Val	Tyr	Glu	Glu	Arg	Gly	Glu	Ala	Gly	Leu
			100					105					110		
Arg	Ala	Leu	Lys	Ile	Gly	Thr	Lys	Arg	Asn	Ile	Ala	Ile	Ser	Val	Asp
			115				120					125			
Pro	Glu	Lys	Ala	Ala	Ser	Ala	Leu	Glu	Leu	Ser	Lys	Asp	Arg	Arg	Ile
	130					135					140				
Glu	Asp	Leu	Glu	Arg	Gln	Val	Arg	Phe	Leu	Glu	Thr	Arg	Leu	Met	Tyr
145					150					155					160
Leu	Lys	Lys	Leu	Lys	Ala	Leu	Ala	His	Pro	Thr	Lys	Lys			
				165					170						

<210> 310
 <211> 283
 <212> PRT
 <213> E. Coli

<400> 310

Met	Lys	Val	Leu	Asn	Glu	Leu	Arg	Gln	Phe	Tyr	Pro	Leu	Asp	Glu	Leu
1				5					10					15	
Leu	Arg	Ala	Ala	Glu	Ile	Pro	Arg	Ser	Thr	Phe	Tyr	Tyr	His	Leu	Lys
			20					25					30		
Ala	Leu	Ser	Lys	Pro	Asp	Lys	Tyr	Ala	Asp	Val	Lys	Lys	Arg	Ile	Ser
		35					40					45			
Glu	Ile	Tyr	His	Glu	Asn	Arg	Gly	Arg	Tyr	Gly	Tyr	Arg	Arg	Val	Thr
	50				55					60					
Leu	Ser	Leu	His	Arg	Glu	Gly	Lys	Gln	Ile	Asn	His	Lys	Ala	Val	Gln
65					70					75					80
Arg	Leu	Met	Gly	Thr	Leu	Ser	Leu	Lys	Ala	Ala	Ile	Lys	Val	Lys	Arg
				85					90					95	
Tyr	Arg	Ser	Tyr	Arg	Gly	Glu	Val	Gly	Gln	Thr	Ala	Pro	Asn	Val	Leu
			100					105					110		
Gln	Arg	Asp	Phe	Lys	Ala	Thr	Arg	Pro	Asn	Glu	Lys	Trp	Val	Thr	Asp
			115				120					125			
Val	Thr	Glu	Phe	Ala	Val	Asn	Gly	Arg	Lys	Leu	Tyr	Leu	Ser	Pro	Val
	130					135					140				
Ile	Asp	Leu	Phe	Asn	Asn	Glu	Val	Ile	Ser	Tyr	Ser	Leu	Ser	Glu	Arg
145					150					155					160
Pro	Val	Met	Asn	Met	Val	Glu	Asn	Met	Leu	Asp	Gln	Ala	Phe	Lys	Lys
				165					170					175	

Leu Asn Pro His Glu His Pro Val Leu His Ser Asp Gln Gly Trp Gln
 180 185 190
 Tyr Arg Met Arg Arg Tyr Gln Asn Ile Leu Lys Glu His Gly Ile Lys
 195 200 205
 Gln Ser Met Ser Arg Lys Gly Asn Cys Leu Asp Asn Ala Val Val Glu
 210 215 220
 Cys Phe Phe Gly Thr Leu Lys Ser Glu Cys Phe Tyr Leu Asp Glu Phe
 225 230 235 240
 Ser Asn Ile Ser Glu Leu Lys Asp Ala Val Thr Glu Tyr Ile Glu Tyr
 245 250 255
 Tyr Asn Ser Arg Arg Ile Ser Leu Lys Leu Lys Gly Leu Thr Pro Ile
 260 265 270
 Glu Tyr Arg Asn Gln Thr Tyr Met Pro Arg Val
 275 280

<210> 311
 <211> 38
 <212> PRT
 <213> E. Coli

<400> 311
 Met Lys Val Arg Ala Ser Val Lys Lys Leu Cys Arg Asn Cys Lys Ile
 1 5 10 15
 Val Lys Arg Asp Gly Val Ile Arg Val Ile Cys Ser Ala Glu Pro Lys
 20 25 30
 His Lys Gln Arg Gln Gly
 35

<210> 312
 <211> 443
 <212> PRT
 <213> E. Coli

<400> 312
 Met Ala Lys Gln Pro Gly Leu Asp Phe Gln Ser Ala Lys Gly Gly Leu
 1 5 10 15
 Gly Glu Leu Lys Arg Arg Leu Leu Phe Val Ile Gly Ala Leu Ile Val
 20 25 30
 Phe Arg Ile Gly Ser Phe Ile Pro Ile Pro Gly Ile Asp Ala Ala Val
 35 40 45
 Leu Ala Lys Leu Leu Glu Gln Arg Gly Thr Ile Ile Glu Met Phe
 50 55 60
 Asn Met Phe Ser Gly Gly Ala Leu Ser Arg Ala Ser Ile Phe Ala Leu
 65 70 75 80
 Gly Ile Met Pro Tyr Ile Ser Ala Ser Ile Ile Ile Gln Leu Leu Thr
 85 90 95
 Val Val His Pro Thr Leu Ala Glu Ile Lys Lys Glu Gly Glu Ser Gly
 100 105 110
 Arg Arg Lys Ile Ser Gln Tyr Thr Arg Tyr Gly Thr Leu Val Leu Ala
 115 120 125
 Ile Phe Gln Ser Ile Gly Ile Ala Thr Gly Leu Pro Asn Met Pro Gly
 130 135 140
 Met Gln Gly Leu Val Ile Asn Pro Gly Phe Ala Phe Tyr Phe Thr Ala
 145 150 155 160
 Val Val Ser Leu Val Thr Gly Thr Met Phe Leu Met Trp Leu Gly Glu
 165 170 175

Gln Ile Thr Glu Arg Gly Ile Gly Asn Gly Ile Ser Ile Ile Ile Phe
 180 185 190
 Ala Gly Ile Val Ala Gly Leu Pro Pro Ala Ile Ala His Thr Ile Glu
 195 200 205
 Gln Ala Arg Gln Gly Asp Leu His Phe Leu Val Leu Leu Leu Val Ala
 210 215 220
 Val Leu Val Phe Ala Val Thr Phe Phe Val Val Phe Val Glu Arg Gly
 225 230 235 240
 Gln Arg Arg Ile Val Val Asn Tyr Ala Lys Arg Gln Gln Gly Arg Arg
 245 250 255
 Val Tyr Ala Ala Gln Ser Thr His Leu Pro Leu Lys Val Asn Met Ala
 260 265 270
 Gly Val Ile Pro Ala Ile Phe Ala Ser Ser Ile Ile Leu Phe Pro Ala
 275 280 285
 Thr Ile Ala Ser Trp Phe Gly Gly Gly Thr Gly Trp Asn Trp Leu Thr
 290 295 300
 Thr Ile Ser Leu Tyr Leu Gln Pro Gly Gln Pro Leu Tyr Val Leu Leu
 305 310 315 320
 Tyr Ala Ser Ala Ile Ile Phe Phe Cys Phe Phe Tyr Thr Ala Leu Val
 325 330 335
 Phe Asn Pro Arg Glu Thr Ala Asp Asn Leu Lys Lys Ser Gly Ala Phe
 340 345 350
 Val Pro Gly Ile Arg Pro Gly Glu Gln Thr Ala Lys Tyr Ile Asp Lys
 355 360 365
 Val Met Thr Arg Leu Thr Leu Val Gly Ala Leu Tyr Ile Thr Phe Ile
 370 375 380
 Cys Leu Ile Pro Glu Phe Met Arg Asp Ala Met Lys Val Pro Phe Tyr
 385 390 395 400
 Phe Gly Gly Thr Ser Leu Leu Ile Val Val Val Ile Met Asp Phe
 405 410 415
 Met Ala Gln Val Gln Thr Leu Met Met Ser Ser Gln Tyr Glu Ser Ala
 420 425 430
 Leu Lys Lys Ala Asn Leu Lys Gly Tyr Gly Arg
 435 440

<210> 313
 <211> 144
 <212> PRT
 <213> E. Coli

<400> 313
 Met Arg Leu Asn Thr Leu Ser Pro Ala Glu Gly Ser Lys Lys Ala Gly
 1 5 10 15
 Lys Arg Leu Gly Arg Gly Ile Gly Ser Gly Leu Gly Lys Thr Gly Gly
 20 25 30
 Arg Gly His Lys Gly Gln Lys Ser Arg Ser Gly Gly Gly Val Arg Arg
 35 40 45
 Gly Phe Glu Gly Gly Gln Met Pro Leu Tyr Arg Arg Leu Pro Lys Phe
 50 55 60
 Gly Phe Thr Ser Arg Lys Ala Ala Ile Thr Ala Glu Ile Arg Leu Ser
 65 70 75 80
 Asp Leu Ala Lys Val Glu Gly Gly Val Val Asp Leu Asn Thr Leu Lys
 85 90 95
 Ala Ala Asn Ile Ile Gly Ile Gln Ile Glu Phe Ala Lys Val Ile Leu
 100 105 110

Ala	Gly	Glu	Val	Thr	Thr	Pro	Val	Thr	Val	Arg	Gly	Leu	Arg	Val	Thr
	115						120					125			
Lys	Gly	Ala	Arg	Ala	Ala	Ile	Glu	Ala	Ala	Gly	Gly	Lys	Ile	Glu	Glu
	130					135					140				

<210> 314
 <211> 59
 <212> PRT
 <213> E. Coli

<400> 314

Met	Ala	Lys	Thr	Ile	Lys	Ile	Thr	Gln	Thr	Arg	Ser	Ala	Ile	Gly	Arg
1				5					10					15	
Leu	Pro	Lys	His	Lys	Ala	Thr	Leu	Leu	Gly	Leu	Gly	Leu	Arg	Arg	Ile
			20					25					30		
Gly	His	Thr	Val	Glu	Arg	Glu	Asp	Thr	Pro	Ala	Ile	Arg	Gly	Met	Ile
		35					40						45		
Asn	Ala	Val	Ser	Phe	Met	Val	Lys	Val	Glu	Glu					
	50					55									

<210> 315
 <211> 167
 <212> PRT
 <213> E. Coli

<400> 315

Met	Ala	His	Ile	Glu	Lys	Gln	Ala	Gly	Glu	Leu	Gln	Glu	Lys	Leu	Ile
1				5					10					15	
Ala	Val	Asn	Arg	Val	Ser	Lys	Thr	Val	Lys	Gly	Gly	Arg	Ile	Phe	Ser
		20						25					30		
Phe	Thr	Ala	Leu	Thr	Val	Val	Gly	Asp	Gly	Asn	Gly	Arg	Val	Gly	Phe
		35					40					45			
Gly	Tyr	Gly	Lys	Ala	Arg	Glu	Val	Pro	Ala	Ala	Ile	Gln	Lys	Ala	Met
	50					55					60				
Glu	Lys	Ala	Arg	Arg	Asn	Met	Ile	Asn	Val	Ala	Leu	Asn	Asn	Gly	Thr
65					70					75				80	
Leu	Gln	His	Pro	Val	Lys	Gly	Val	His	Thr	Gly	Ser	Arg	Val	Phe	Met
			85						90					95	
Gln	Pro	Ala	Ser	Glu	Gly	Thr	Gly	Ile	Ile	Ala	Gly	Gly	Ala	Met	Arg
			100					105					110		
Ala	Val	Leu	Glu	Val	Ala	Gly	Val	His	Asn	Val	Leu	Ala	Lys	Ala	Tyr
		115					120					125			
Gly	Ser	Thr	Asn	Pro	Ile	Asn	Val	Val	Arg	Ala	Thr	Ile	Asp	Gly	Leu
	130					135					140				
Glu	Asn	Met	Asn	Ser	Pro	Glu	Met	Val	Ala	Ala	Lys	Arg	Gly	Lys	Ser
145					150					155					160
Val	Glu	Glu	Ile	Leu	Gly	Lys									
				165											

<210> 316
 <211> 117
 <212> PRT
 <213> E. Coli

<400> 316
Met Asp Lys Lys Ser Ala Arg Ile Arg Arg Ala Thr Arg Ala Arg Arg
1 5 10 15
Lys Leu Gln Glu Leu Gly Ala Thr Arg Leu Val Val His Arg Thr Pro
20 25 30
Arg His Ile Tyr Ala Gln Val Ile Ala Pro Asn Gly Ser Glu Val Leu
35 40 45
Val Ala Ala Ser Thr Val Glu Lys Ala Ile Ala Glu Gln Leu Lys Tyr
50 55 60
Thr Gly Asn Lys Asp Ala Ala Ala Val Gly Lys Ala Val Ala Glu
65 70 75 80
Arg Ala Leu Glu Lys Gly Ile Lys Asp Val Ser Phe Asp Arg Ser Gly
85 90 95
Phe Gln Tyr His Gly Arg Val Gln Ala Leu Ala Asp Ala Ala Arg Glu
100 105 110
Ala Gly Leu Gln Phe
115

<210> 317
<211> 177
<212> PRT
<213> E. Coli

<400> 317
Met Ser Arg Val Ala Lys Ala Pro Val Val Val Pro Ala Gly Val Asp
1 5 10 15
Val Lys Ile Asn Gly Gln Val Ile Thr Lys Gly Lys Asn Gly Glu
20 25 30
Leu Thr Arg Thr Leu Asn Asp Ala Val Glu Val Lys His Ala Asp Asn
35 40 45
Thr Leu Thr Phe Gly Pro Arg Asp Gly Tyr Ala Asp Gly Trp Ala Gln
50 55 60
Ala Gly Thr Ala Arg Ala Leu Leu Asn Ser Met Val Ile Gly Val Thr
65 70 75 80
Glu Gly Phe Thr Lys Lys Leu Gln Leu Val Gly Val Gly Tyr Arg Ala
85 90 95
Ala Val Lys Gly Asn Val Ile Asn Leu Ser Leu Gly Phe Ser His Pro
100 105 110
Val Asp His Gln Leu Pro Ala Gly Ile Thr Ala Glu Cys Pro Thr Gln
115 120 125
Thr Glu Ile Val Leu Lys Gly Ala Asp Lys Gln Val Ile Gly Gln Val
130 135 140
Ala Ala Asp Leu Arg Ala Tyr Arg Arg Pro Glu Pro Tyr Lys Gly Lys
145 150 155 160
Gly Val Arg Tyr Ala Asp Glu Val Val Arg Thr Lys Glu Ala Lys Lys
165 170 175
Lys

<210> 318
<211> 130
<212> PRT
<213> E. Coli

<400> 318

Met	Ser	Met	Gln	Asp	Pro	Ile	Ala	Asp	Met	Leu	Thr	Arg	Ile	Arg	Asn
1				5					10					15	
Gly	Gln	Ala	Ala	Asn	Lys	Ala	Ala	Val	Thr	Met	Pro	Ser	Ser	Lys	Leu
		20						25					30		
Lys	Val	Ala	Ile	Ala	Asn	Val	Leu	Lys	Glu	Glu	Gly	Phe	Ile	Glu	Asp
	35						40					45			
Phe	Lys	Val	Glu	Gly	Asp	Thr	Lys	Pro	Glu	Leu	Glu	Leu	Thr	Leu	Lys
	50					55					60				
Tyr	Phe	Gln	Gly	Lys	Ala	Val	Val	Glu	Ser	Ile	Gln	Arg	Val	Ser	Arg
65					70					75					80
Pro	Gly	Leu	Arg	Ile	Tyr	Lys	Arg	Lys	Asp	Glu	Leu	Pro	Lys	Val	Met
				85					90					95	
Ala	Gly	Leu	Gly	Ile	Ala	Val	Val	Ser	Thr	Ser	Lys	Gly	Val	Met	Thr
			100					105					110		
Asp	Arg	Ala	Ala	Arg	Gln	Ala	Gly	Leu	Gly	Gly	Glu	Ile	Ile	Cys	Tyr
		115					120					125			
Val	Ala														
															130

<210> 319
 <211> 101
 <212> PRT
 <213> E. Coli

<400> 319

Met	Ala	Lys	Gln	Ser	Met	Lys	Ala	Arg	Glu	Val	Lys	Arg	Val	Ala	Leu
1				5					10					15	
Ala	Asp	Lys	Tyr	Phe	Ala	Lys	Arg	Ala	Glu	Leu	Lys	Ala	Ile	Ile	Ser
		20						25					30		
Asp	Val	Asn	Ala	Ser	Asp	Glu	Asp	Arg	Trp	Asn	Ala	Val	Leu	Lys	Leu
		35					40					45			
Gln	Thr	Leu	Pro	Arg	Asp	Ser	Ser	Pro	Ser	Arg	Gln	Arg	Asn	Arg	Cys
	50					55					60				
Arg	Gln	Thr	Gly	Arg	Pro	His	Gly	Phe	Leu	Arg	Lys	Phe	Gly	Leu	Ser
65					70					75					80
Arg	Ile	Lys	Val	Arg	Glu	Ala	Ala	Met	Arg	Gly	Glu	Ile	Pro	Gly	Leu
				85					90					95	
Lys	Lys	Ala	Ser	Trp											
				100											

<210> 320
 <211> 179
 <212> PRT
 <213> E. Coli

<400> 320

Met	Ala	Lys	Leu	His	Asp	Tyr	Tyr	Lys	Asp	Glu	Val	Val	Lys	Lys	Leu
1				5					10					15	
Met	Thr	Glu	Phe	Asn	Tyr	Asn	Ser	Val	Met	Gln	Val	Pro	Arg	Val	Glu
		20						25					30		
Lys	Ile	Thr	Leu	Asn	Met	Gly	Val	Gly	Glu	Ala	Ile	Ala	Asp	Lys	Lys
	35					40						45			
Leu	Leu	Asp	Asn	Ala	Ala	Ala	Asp	Leu	Ala	Ala	Ile	Ser	Gly	Gln	Lys

50		55		60											
Pro	Leu	Ile	Thr	Lys	Ala	Arg	Lys	Ser	Val	Ala	Gly	Phe	Lys	Ile	Arg
65					70					75					80
Gln	Gly	Tyr	Pro	Ile	Gly	Cys	Lys	Val	Thr	Leu	Arg	Gly	Glu	Arg	Met
				85					90						95
Trp	Glu	Phe	Phe	Glu	Arg	Leu	Ile	Thr	Ile	Ala	Val	Pro	Arg	Ile	Arg
			100					105					110		
Asp	Phe	Arg	Gly	Leu	Ser	Ala	Lys	Ser	Phe	Asp	Gly	Arg	Gly	Asn	Tyr
		115					120					125			
Ser	Met	Gly	Val	Arg	Glu	Gln	Ile	Ile	Phe	Pro	Glu	Ile	Asp	Tyr	Asp
	130					135					140				
Lys	Val	Asp	Arg	Val	Arg	Gly	Leu	Asp	Ile	Thr	Ile	Thr	Thr	Thr	Ala
145					150					155					160
Lys	Ser	Asp	Glu	Glu	Gly	Arg	Ala	Leu	Leu	Ala	Ala	Phe	Asp	Phe	Pro
			165					170						175	
Phe	Arg	Lys													

<210> 321Z
 <211> 104
 <212> PRT
 <213> E. Coli

<400> 321															
Met	Ala	Ala	Lys	Ile	Arg	Arg	Asp	Asp	Glu	Val	Ile	Val	Leu	Thr	Gly
1				5					10					15	
Lys	Asp	Lys	Gly	Lys	Arg	Gly	Lys	Val	Lys	Asn	Val	Leu	Ser	Ser	Gly
			20					25					30		
Lys	Val	Ile	Val	Glu	Gly	Ile	Asn	Leu	Val	Lys	Lys	His	Gln	Lys	Pro
		35					40					45			
Val	Pro	Ala	Leu	Asn	Gln	Pro	Gly	Gly	Ile	Val	Glu	Lys	Glu	Ala	Ala
	50					55					60				
Ile	Gln	Val	Ser	Asn	Val	Ala	Ile	Phe	Asn	Ala	Ala	Thr	Gly	Lys	Ala
65				70					75						80
Asp	Arg	Val	Gly	Phe	Arg	Phe	Glu	Asp	Gly	Lys	Lys	Val	Arg	Phe	Phe
			85						90					95	
Lys	Ser	Asn	Ser	Glu	Thr	Ile	Lys								
			100												

<210> 322
 <211> 123
 <212> PRT
 <213> E. Coli

<400> 322															
Met	Ile	Gln	Glu	Gln	Thr	Met	Leu	Asn	Val	Ala	Asp	Asn	Ser	Gly	Ala
1				5					10					15	
Arg	Arg	Val	Met	Cys	Ile	Lys	Val	Leu	Gly	Gly	Ser	His	Arg	Arg	Tyr
			20					25					30		
Ala	Gly	Val	Gly	Asp	Ile	Ile	Lys	Ile	Thr	Ile	Lys	Glu	Ala	Ile	Pro
		35					40					45			
Arg	Gly	Lys	Val	Lys	Lys	Gly	Asp	Val	Leu	Lys	Ala	Val	Val	Val	Arg
	50					55					60				
Thr	Lys	Lys	Gly	Val	Arg	Arg	Pro	Asp	Gly	Ser	Val	Ile	Arg	Phe	Asp
65				70					75						80

Gly Asn Ala Cys Val Leu Leu Asn Asn Asn Ser Glu Gln Pro Ile Gly
 85 90 95
 Thr Arg Ile Phe Gly Pro Val Thr Arg Glu Leu Arg Ser Glu Lys Phe
 100 105 110
 Met Lys Ile Ile Ser Leu Ala Pro Glu Val Leu
 115 120

<210> 323
 <211> 188
 <212> PRT
 <213> E. Coli

<400> 323
 Met Phe Lys Gly Gln Lys Thr Leu Ala Ala Leu Ala Val Ser Leu Leu
 1 5 10 15
 Phe Thr Ala Pro Val Tyr Ala Ala Asp Glu Gly Ser Gly Glu Ile His
 20 25 30
 Phe Lys Gly Glu Val Ile Glu Ala Pro Cys Glu Ile His Pro Glu Asp
 35 40 45
 Ile Asp Lys Asn Ile Asp Leu Gly Gln Val Thr Thr Thr His Ile Asn
 50 55 60
 Arg Glu His His Ser Asn Lys Val Ala Val Asp Ile Arg Leu Ile Asn
 65 70 75 80
 Cys Asp Leu Pro Ala Ser Asp Asn Gly Ser Gly Met Pro Val Ser Lys
 85 90 95
 Val Gly Val Thr Phe Asp Ser Thr Ala Lys Thr Thr Gly Ala Thr Pro
 100 105 110
 Leu Leu Ser Asn Thr Ser Ala Gly Glu Ala Thr Gly Val Gly Val Arg
 115 120 125
 Leu Met Asp Lys Asn Asp Gly Asn Ile Val Leu Gly Ser Ala Ala Pro
 130 135 140
 Asp Leu Asp Leu Asp Ala Ser Ser Ser Glu Gln Thr Leu Asn Phe Phe
 145 150 155 160
 Ala Trp Met Glu Gln Ile Asp Asn Ala Val Asp Val Thr Ala Gly Glu
 165 170 175
 Val Thr Ala Asn Ala Thr Tyr Val Leu Asp Tyr Lys
 180 185

<210> 324
 <211> 427
 <212> PRT
 <213> E. Coli

<400> 324
 Met Ala Asp Thr Lys Ala Lys Leu Thr Leu Asn Gly Asp Thr Ala Val
 1 5 10 15
 Glu Leu Asp Val Leu Lys Gly Thr Leu Gly Gln Asp Val Ile Asp Ile
 20 25 30
 Arg Thr Leu Gly Ser Lys Gly Val Phe Thr Phe Asp Pro Gly Phe Thr
 35 40 45
 Ser Thr Ala Ser Cys Glu Ser Lys Ile Thr Phe Ile Asp Gly Asp Glu
 50 55 60
 Gly Ile Leu Leu His Arg Gly Phe Pro Ile Asp Gln Leu Ala Thr Asp
 65 70 75 80
 Ser Asn Tyr Leu Glu Val Cys Tyr Ile Leu Leu Asn Gly Glu Lys Pro

Arg	Pro	Gly	Gly	Ala	Ala	Asn	Val	Ala	Met	Asn	Ile	Ala	Ser	Leu	Gly
50						55					60				
Ala	Asn	Ala	Arg	Leu	Val	Gly	Leu	Thr	Gly	Ile	Asp	Asp	Ala	Ala	Arg
65					70					75					80
Ala	Leu	Ser	Lys	Ser	Leu	Ala	Asp	Val	Asn	Val	Lys	Cys	Asp	Phe	Val
				85					90					95	
Ser	Val	Pro	Thr	His	Pro	Thr	Ile	Thr	Lys	Leu	Arg	Val	Leu	Ser	Arg
			100					105					110		
Asn	Gln	Gln	Leu	Ile	Arg	Leu	Asp	Phe	Glu	Glu	Gly	Phe	Glu	Gly	Val
		115					120					125			
Asp	Pro	Gln	Pro	Leu	His	Glu	Arg	Ile	Asn	Gln	Ala	Leu	Ser	Ser	Ile
	130					135					140				
Gly	Ala	Leu	Val	Leu	Ser	Asp	Tyr	Ala	Lys	Gly	Ala	Leu	Ala	Ser	Val
145					150					155					160
Gln	Gln	Met	Ile	Gln	Leu	Ala	Arg	Lys	Ala	Gly	Val	Pro	Val	Leu	Ile
				165					170					175	
Asp	Pro	Lys	Gly	Thr	Asp	Phe	Glu	Arg	Tyr	Arg	Gly	Ala	Thr	Leu	Leu
			180					185					190		
Thr	Pro	Asn	Leu	Ser	Glu	Phe	Glu	Ala	Val	Val	Gly	Lys	Cys	Lys	Thr
			195					200					205		
Glu	Glu	Glu	Ile	Val	Glu	Arg	Gly	Met	Lys	Leu	Ile	Ala	Asp	Tyr	Glu
		210					215					220			
Leu	Ser	Ala	Leu	Leu	Val	Thr	Arg	Ser	Glu	Gln	Gly	Met	Ser	Leu	Leu
225					230						235				240
Gln	Pro	Gly	Lys	Ala	Pro	Leu	His	Met	Pro	Thr	Gln	Ala	Gln	Glu	Val
				245					250					255	
Tyr	Asp	Val	Thr	Gly	Ala	Gly	Asp	Thr	Val	Ile	Gly	Val	Leu	Ala	Ala
			260					265					270		
Thr	Leu	Ala	Ala	Gly	Asn	Ser	Leu	Glu	Glu	Ala	Cys	Phe	Phe	Ala	Asn
		275					280						285		
Ala	Ala	Ala	Gly	Val	Val	Val	Gly	Lys	Leu	Gly	Thr	Ser	Thr	Val	Ser
		290					295					300			
Pro	Ile	Glu	Leu	Glu	Asn	Ala	Val	Arg	Gly	Arg	Ala	Asp	Thr	Gly	Phe
305					310					315					320
Gly	Val	Met	Thr	Glu	Glu	Glu	Leu	Lys	Leu	Ala	Val	Ala	Ala	Ala	Arg
				325					330					335	
Lys	Arg	Gly	Glu	Lys	Val	Val	Met	Thr	Asn	Gly	Val	Phe	Asp	Ile	Leu
			340					345					350		
His	Ala	Gly	His	Val	Ser	Tyr	Leu	Ala	Asn	Ala	Arg	Lys	Leu	Gly	Asp
		355					360						365		
Arg	Leu	Ile	Val	Ala	Val	Asn	Ser	Asp	Ala	Ser	Thr	Lys	Arg	Leu	Lys
	370					375							380		
Gly	Asp	Ser	Arg	Pro	Val	Asn	Pro	Leu	Glu	Gln	Arg	Met	Ile	Val	Leu
385					390					395					400
Gly	Ala	Leu	Glu	Ala	Val	Asp	Trp	Val	Val	Ser	Phe	Glu	Glu	Asp	Thr
				405					410					415	
Pro	Gln	Arg	Leu	Ile	Ala	Gly	Ile	Leu	Pro	Asp	Leu	Leu	Val	Lys	Gly
			420					425					430		
Gly	Asp	Tyr	Lys	Pro	Glu	Glu	Ile	Ala	Gly	Ser	Lys	Glu	Val	Trp	Ala
		435					440					445			
Asn	Gly	Gly	Glu	Val	Leu	Val	Leu	Asn	Phe	Glu	Asp	Gly	Cys	Ser	Thr
	450					455					460				
Thr	Asn	Ile	Ile	Lys	Lys	Ile	Gln	Gln	Asp	Lys	Lys	Gly			
465					470					475					

<210> 326

<211> 946
 <212> PRT
 <213> E. Coli

<400> 326

Met	Lys	Pro	Leu	Ser	Ser	Pro	Leu	Gln	Gln	Tyr	Trp	Gln	Thr	Val	Val		
1				5					10					15			
Glu	Arg	Leu	Pro	Glu	Pro	Leu	Ala	Glu	Glu	Ser	Leu	Ser	Ala	Gln	Ala		
			20					25					30				
Lys	Ser	Val	Leu	Thr	Phe	Ser	Asp	Phe	Val	Gln	Asp	Ser	Val	Ile	Ala		
		35					40					45					
His	Pro	Glu	Trp	Leu	Thr	Glu	Leu	Glu	Ser	Gln	Pro	Pro	Gln	Ala	Asp		
	50					55					60						
Glu	Trp	Gln	His	Tyr	Ala	Ala	Trp	Leu	Gln	Glu	Ala	Leu	Cys	Asn	Val		
65					70					75					80		
Ser	Asp	Glu	Ala	Gly	Leu	Met	Arg	Glu	Leu	Arg	Leu	Phe	Arg	Arg	Arg		
				85					90					95			
Ile	Met	Val	Arg	Ile	Ala	Trp	Ala	Gln	Thr	Leu	Ala	Leu	Val	Thr	Glu		
		100						105					110				
Glu	Ser	Ile	Leu	Gln	Gln	Leu	Ser	Tyr	Leu	Ala	Glu	Thr	Leu	Ile	Val		
		115					120					125					
Ala	Ala	Arg	Asp	Trp	Leu	Tyr	Asp	Ala	Cys	Cys	Arg	Glu	Trp	Gly	Thr		
	130					135					140						
Pro	Cys	Asn	Ala	Gln	Gly	Glu	Ala	Gln	Pro	Leu	Leu	Ile	Leu	Gly	Met		
145					150					155					160		
Gly	Lys	Leu	Gly	Gly	Gly	Glu	Leu	Asn	Phe	Ser	Ser	Asp	Ile	Asp	Leu		
			165						170					175			
Ile	Phe	Ala	Trp	Pro	Glu	His	Gly	Cys	Thr	Gln	Gly	Gly	Arg	Arg	Glu		
		180						185					190				
Leu	Asp	Asn	Ala	Gln	Phe	Phe	Thr	Arg	Met	Gly	Gln	Arg	Leu	Ile	Lys		
		195					200					205					
Val	Leu	Asp	Gln	Pro	Thr	Gln	Asp	Gly	Phe	Val	Tyr	Arg	Val	Asp	Met		
	210					215					220						
Arg	Leu	Arg	Pro	Phe	Gly	Glu	Ser	Gly	Pro	Leu	Val	Leu	Ser	Phe	Ala		
225					230					235					240		
Ala	Leu	Glu	Asp	Tyr	Tyr	Gln	Glu	Gln	Gly	Arg	Asp	Trp	Glu	Arg	Tyr		
				245					250					255			
Ala	Met	Val	Lys	Ala	Arg	Ile	Met	Gly	Asp	Ser	Glu	Gly	Val	Tyr	Ala		
		260						265					270				
Asn	Glu	Leu	Arg	Ala	Met	Leu	Arg	Pro	Phe	Val	Phe	Arg	Arg	Tyr	Ile		
	275					280						285					
Asp	Phe	Ser	Val	Ile	Gln	Ser	Leu	Arg	Asn	Met	Lys	Gly	Met	Ile	Ala		
	290					295					300						
Arg	Glu	Val	Arg	Arg	Arg	Gly	Leu	Thr	Asp	Asn	Ile	Lys	Leu	Gly	Ala		
305					310					315					320		
Gly	Gly	Ile	Arg	Glu	Ile	Glu	Phe	Ile	Val	Gln	Val	Phe	Gln	Leu	Ile		
				325					330				335				
Arg	Gly	Gly	Arg	Glu	Pro	Ser	Leu	Gln	Ser	Arg	Ser	Leu	Leu	Pro	Thr		
			340					345					350				
Leu	Ser	Ala	Ile	Ala	Glu	Leu	His	Leu	Leu	Ser	Glu	Asn	Asp	Ala	Glu		
		355					360					365					
Gln	Leu	Arg	Val	Ala	Tyr	Leu	Phe	Leu	Arg	Arg	Leu	Glu	Asn	Leu	Leu		
	370					375					380						
Gln	Ser	Ile	Asn	Asp	Glu	Gln	Thr	Gln	Thr	Leu	Pro	Ser	Asp	Glu	Leu		
385					390					395					400		
Asn	Arg	Ala	Arg	Leu	Ala	Trp	Ala	Met	Asp	Phe	Ala	Asp	Trp	Pro	Gln		
			405						410					415			

Leu	Thr	Gly	Ala	Leu	Thr	Ala	His	Met	Thr	Asn	Val	Arg	Arg	Val	Phe
			420					425						430	
Asn	Glu	Leu	Ile	Gly	Asp	Asp	Glu	Ser	Glu	Thr	Gln	Glu	Glu	Ser	Leu
		435					440					445			
Ser	Glu	Gln	Trp	Arg	Glu	Leu	Trp	Gln	Asp	Ala	Leu	Gln	Glu	Asp	Asp
	450					455					460				
Thr	Thr	Pro	Val	Leu	Ala	His	Leu	Ser	Glu	Asp	Asp	Arg	Lys	Gln	Val
465					470					475					480
Leu	Thr	Leu	Ile	Ala	Asp	Phe	Arg	Lys	Glu	Leu	Asp	Lys	Arg	Thr	Ile
			485						490					495	
Gly	Pro	Arg	Gly	Arg	Gln	Val	Leu	Asp	His	Leu	Met	Pro	His	Leu	Leu
			500					505					510		
Ser	Asp	Val	Cys	Ala	Arg	Glu	Asp	Ala	Ala	Val	Thr	Leu	Ser	Arg	Ile
		515					520					525			
Thr	Ala	Leu	Leu	Val	Gly	Ile	Val	Thr	Arg	Thr	Thr	Tyr	Leu	Glu	Leu
	530				535						540				
Leu	Ser	Glu	Phe	Pro	Ala	Ala	Leu	Lys	His	Leu	Ile	Ser	Leu	Cys	Ala
545					550					555					560
Ala	Ser	Pro	Met	Ile	Ala	Ser	Gln	Leu	Ala	Arg	Tyr	Pro	Leu	Leu	Leu
			565						570					575	
Asp	Glu	Leu	Leu	Asp	Pro	Asn	Thr	Leu	Tyr	Gln	Pro	Thr	Ala	Thr	Asp
			580					585					590		
Ala	Tyr	Arg	Asp	Glu	Leu	Arg	Gln	Tyr	Leu	Leu	Arg	Val	Pro	Glu	Asp
	595						600					605			
Asp	Glu	Glu	Gln	Gln	Leu	Glu	Ala	Leu	Arg	Gln	Phe	Lys	Gln	Ala	Gln
	610					615					620				
Leu	Leu	Arg	Ile	Ala	Ala	Ala	Asp	Ile	Ala	Gly	Thr	Leu	Pro	Val	Met
625					630					635					640
Lys	Val	Ser	Asp	His	Leu	Thr	Trp	Leu	Ala	Glu	Ala	Met	Ile	Asp	Ala
			645						650					655	
Val	Val	Gln	Gln	Ala	Trp	Val	Gln	Met	Val	Ala	Arg	Tyr	Gly	Lys	Pro
			660					665					670		
Asn	His	Leu	Asn	Glu	Arg	Glu	Gly	Arg	Gly	Phe	Ala	Val	Val	Gly	Tyr
		675					680					685			
Gly	Lys	Leu	Gly	Gly	Trp	Glu	Leu	Gly	Tyr	Ser	Ser	Asp	Leu	Asp	Leu
	690					695					700				
Ile	Phe	Leu	His	Asp	Cys	Pro	Met	Asp	Ala	Met	Thr	Asp	Gly	Glu	Arg
705					710					715					720
Glu	Ile	Asp	Gly	Arg	Gln	Phe	Tyr	Leu	Arg	Leu	Ala	Gln	Arg	Ile	Met
			725						730					735	
His	Leu	Phe	Ser	Thr	Arg	Thr	Ser	Ser	Gly	Ile	Leu	Tyr	Glu	Val	Asp
			740					745					750		
Ala	Arg	Leu	Arg	Pro	Ser	Gly	Ala	Ala	Gly	Met	Leu	Val	Thr	Ser	Ala
		755					760					765			
Glu	Ala	Phe	Ala	Asp	Tyr	Gln	Lys	Asn	Glu	Ala	Trp	Thr	Trp	Glu	His
	770					775					780				
Gln	Ala	Leu	Val	Arg	Ala	Arg	Val	Val	Tyr	Gly	Asp	Pro	Gln	Leu	Thr
785					790					795					800
Ala	His	Phe	Asp	Ala	Val	Arg	Arg	Glu	Ile	Met	Thr	Leu	Pro	Arg	Glu
			805						810					815	
Gly	Lys	Thr	Leu	Gln	Thr	Glu	Val	Arg	Glu	Met	Arg	Glu	Lys	Met	Arg
		820						825				830			
Ala	His	Leu	Gly	Asn	Lys	His	Arg	Asp	Arg	Phe	Asp	Ile	Lys	Ala	Asp
		835					840					845			
Glu	Gly	Gly	Ile	Thr	Asp	Ile	Glu	Phe	Ile	Thr	Gln	Tyr	Leu	Val	Leu
850						855					860				
Arg	Tyr	Ala	His	Glu	Lys	Pro	Lys	Leu	Thr	Arg	Trp	Ser	Asp	Asn	Val

865		870		875		880									
Arg	Ile	Leu	Glu	Leu	Leu	Ala	Gln	Asn	Asp	Ile	Met	Glu	Glu	Gln	Glu
		885		890		895									
Ala	Met	Ala	Leu	Thr	Arg	Ala	Tyr	Thr	Thr	Leu	Arg	Asp	Glu	Leu	His
		900		905		910									
His	Leu	Ala	Leu	Gln	Glu	Leu	Pro	Gly	His	Val	Ser	Glu	Asp	Cys	Phe
		915		920		925									
Thr	Ala	Glu	Arg	Glu	Leu	Val	Arg	Ala	Ser	Trp	Gln	Lys	Trp	Leu	Val
		930		935		940									
Glu	Glu														
945															

<210> 327
 <211> 433
 <212> PRT
 <213> E. Coli

<400> 327

Met	Ala	Gln	Glu	Ile	Glu	Leu	Lys	Phe	Ile	Val	Asn	His	Ser	Ala	Val
1				5					10					15	
Glu	Ala	Leu	Arg	Asp	His	Leu	Asn	Thr	Leu	Gly	Gly	Glu	His	His	Asp
			20					25					30		
Pro	Val	Gln	Leu	Leu	Asn	Ile	Tyr	Tyr	Glu	Thr	Pro	Asp	Asn	Trp	Leu
		35					40					45			
Arg	Gly	His	Asp	Met	Gly	Leu	Arg	Ile	Arg	Gly	Glu	Asn	Gly	Arg	Tyr
	50				55						60				
Glu	Met	Thr	Met	Lys	Val	Ala	Gly	Arg	Val	Thr	Gly	Gly	Leu	His	Gln
65				70					75						80
Arg	Pro	Glu	Tyr	Asn	Val	Ala	Leu	Ser	Glu	Pro	Thr	Leu	Asp	Leu	Ala
				85					90					95	
Gln	Leu	Pro	Thr	Glu	Val	Trp	Pro	Asn	Gly	Glu	Leu	Pro	Ala	Asp	Leu
		100						105					110		
Ala	Ser	Arg	Val	Gln	Pro	Leu	Phe	Ser	Thr	Asp	Phe	Tyr	Arg	Glu	Lys
	115						120					125			
Trp	Leu	Val	Ala	Val	Asp	Gly	Ser	Gln	Ile	Glu	Ile	Ala	Leu	Asp	Gln
	130					135					140				
Gly	Glu	Val	Lys	Ala	Gly	Glu	Phe	Ala	Glu	Pro	Ile	Cys	Glu	Leu	Glu
145				150					155						160
Leu	Glu	Leu	Leu	Ser	Gly	Asp	Thr	Arg	Ala	Val	Leu	Lys	Leu	Ala	Asn
			165					170						175	
Gln	Leu	Val	Ser	Gln	Thr	Gly	Leu	Arg	Gln	Gly	Ser	Leu	Ser	Lys	Ala
	180							185					190		
Ala	Arg	Gly	Tyr	His	Leu	Ala	Gln	Gly	Asn	Pro	Ala	Arg	Glu	Ile	Lys
	195						200					205			
Pro	Thr	Thr	Ile	Leu	His	Val	Ala	Ala	Lys	Ala	Asp	Val	Glu	Gln	Gly
	210					215					220				
Leu	Glu	Ala	Ala	Leu	Glu	Leu	Ala	Leu	Ala	Gln	Trp	Gln	Tyr	His	Glu
225				230					235						240
Glu	Leu	Trp	Val	Arg	Gly	Asn	Asp	Ala	Ala	Lys	Glu	Gln	Val	Leu	Ala
			245					250						255	
Ala	Ile	Ser	Leu	Val	Arg	His	Thr	Leu	Met	Leu	Phe	Gly	Gly	Ile	Val
	260						265					270			
Pro	Arg	Lys	Ala	Ser	Thr	His	Leu	Arg	Asp	Leu	Leu	Thr	Gln	Cys	Glu
	275					280						285			
Ala	Thr	Ile	Ala	Ser	Ala	Val	Ser	Ala	Val	Thr	Ala	Val	Tyr	Ser	Thr

290		295		300
Glu Thr Ala Met Ala Lys	Leu Ala Leu Thr	Glu Trp Leu Val Ser Lys		
305	310	315		320
Ala Trp Gln Pro Phe Leu Asp Ala Lys	Ala Gln Gly Lys Ile Ser Asp			
	325	330		335
Ser Phe Lys Arg Phe Ala Asp Ile His Leu Ser Arg His Ala Ala Glu				
	340	345		350
Leu Lys Ser Val Phe Cys Gln Pro Leu Gly Asp Arg Tyr Arg Asp Gln				
	355	360		365
Leu Pro Arg Leu Thr Arg Asp Ile Asp Ser Ile Leu Leu Ala Gly				
	370	375		380
Tyr Tyr Asp Pro Val Val Ala Gln Ala Trp Leu Glu Asn Trp Gln Gly				
385	390	395		400
Leu His His Ala Ile Ala Thr Gly Gln Arg Ile Glu Ile Glu His Phe				
	405	410		415
Arg Asn Glu Ala Asn Asn Gln Glu Pro Phe Trp Leu His Ser Gly Lys				
	420	425		430

Arg

<210> 328
 <211> 70
 <212> PRT
 <213> E. Coli

<400> 328
Met Ser Gly Lys Met Thr Gly Ile Val Lys Trp Phe Asn Ala Asp Lys
1 5 10 15
Gly Phe Gly Phe Ile Thr Pro Asp Asp Gly Ser Lys Asp Val Phe Val
20 25 30
His Phe Ser Ala Ile Gln Asn Asp Gly Tyr Lys Ser Leu Asp Glu Gly
35 40 45
Gln Lys Val Ser Phe Thr Ile Glu Ser Gly Ala Lys Gly Pro Ala Ala
50 55 60
Gly Asn Val Thr Ser Leu
65 70

<210> 329
 <211> 523
 <212> PRT
 <213> E. Coli

<400> 329
Met Arg Asp Ile Val Asp Pro Val Phe Ser Ile Gly Ile Ser Ser Leu
1 5 10 15
Trp Asp Glu Leu Arg His Met Pro Ala Gly Gly Val Trp Trp Phe Asn
20 25 30
Val Asp Arg His Glu Asp Ala Ile Ser Leu Ala Asn Gln Thr Ile Ala
35 40 45
Ser Gln Ala Glu Thr Ala His Val Ala Val Ile Ser Met Asp Ser Asp
50 55 60
Pro Ala Lys Ile Phe Gln Leu Asp Asp Ser Gln Gly Pro Glu Lys Ile
65 70 75 80

Lys	Leu	Phe	Ser	Met	Leu	Asn	His	Glu	Lys	Gly	Leu	Tyr	Tyr	Leu	Thr
			85						90					95	
Arg	Asp	Leu	Gln	Cys	Ser	Ile	Asp	Pro	His	Asn	Tyr	Leu	Phe	Ile	Leu
		100						105					110		
Val	Cys	Ala	Asn	Asn	Ala	Trp	Gln	Asn	Ile	Pro	Ala	Glu	Arg	Leu	Arg
		115					120					125			
Ser	Trp	Leu	Asp	Lys	Met	Asn	Lys	Trp	Ser	Arg	Leu	Asn	His	Cys	Ser
	130					135					140				
Leu	Leu	Val	Ile	Asn	Pro	Gly	Asn	Asn	Asn	Asp	Lys	Gln	Phe	Ser	Leu
145				150						155					160
Leu	Leu	Glu	Glu	Tyr	Arg	Ser	Leu	Phe	Gly	Leu	Ala	Ser	Leu	Arg	Phe
			165						170					175	
Gln	Gly	Asp	Gln	His	Leu	Leu	Asp	Ile	Ala	Phe	Trp	Cys	Asn	Glu	Lys
			180					185					190		
Gly	Val	Ser	Ala	Arg	Gln	Gln	Leu	Ser	Val	Gln	Gln	Gln	Asn	Gly	Ile
	195						200					205			
Trp	Thr	Leu	Val	Gln	Ser	Glu	Glu	Ala	Glu	Ile	Gln	Pro	Arg	Ser	Asp
	210					215						220			
Glu	Lys	Arg	Ile	Leu	Ser	Asn	Val	Ala	Val	Leu	Glu	Gly	Ala	Pro	Pro
225				230						235					240
Leu	Ser	Glu	His	Trp	Gln	Leu	Phe	Asn	Asn	Asn	Glu	Val	Leu	Phe	Asn
			245						250					255	
Glu	Ala	Arg	Thr	Ala	Gln	Ala	Ala	Thr	Val	Val	Phe	Ser	Leu	Gln	Gln
		260						265					270		
Asn	Ala	Gln	Ile	Glu	Pro	Leu	Ala	Arg	Ser	Ile	His	Thr	Leu	Arg	Arg
	275						280					285			
Gln	Arg	Gly	Ser	Ala	Met	Lys	Ile	Leu	Val	Arg	Glu	Asn	Thr	Ala	Ser
	290					295					300				
Leu	Arg	Ala	Thr	Asp	Glu	Arg	Leu	Leu	Leu	Ala	Cys	Gly	Ala	Asn	Met
305				310						315					320
Val	Ile	Pro	Trp	Asn	Ala	Pro	Leu	Ser	Arg	Cys	Leu	Thr	Met	Ile	Glu
			325						330					335	
Ser	Val	Gln	Gly	Gln	Lys	Phe	Ser	Arg	Tyr	Val	Pro	Glu	Asp	Ile	Thr
		340						345					350		
Thr	Leu	Leu	Ser	Met	Thr	Gln	Pro	Leu	Lys	Leu	Arg	Gly	Phe	Gln	Lys
	355					360						365			
Trp	Asp	Val	Phe	Cys	Asn	Ala	Val	Asn	Asn	Met	Met	Asn	Asn	Pro	Leu
	370					375					380				
Leu	Pro	Ala	His	Gly	Lys	Gly	Val	Leu	Val	Ala	Leu	Arg	Pro	Val	Pro
385				390						395					400
Gly	Ile	Arg	Val	Glu	Gln	Ala	Leu	Thr	Leu	Cys	Arg	Pro	Asn	Arg	Thr
			405						410					415	
Gly	Asp	Ile	Met	Thr	Ile	Gly	Gly	Asn	Arg	Leu	Val	Leu	Phe	Leu	Ser
		420						425					430		
Phe	Cys	Arg	Ile	Asn	Asp	Leu	Asp	Thr	Ala	Leu	Asn	His	Ile	Phe	Pro
	435					440						445			
Leu	Pro	Thr	Gly	Asp	Ile	Phe	Ser	Asn	Arg	Met	Val	Trp	Phe	Glu	Asp
	450					455					460				
Asp	Gln	Ile	Ser	Ala	Glu	Leu	Val	Gln	Met	Arg	Leu	Leu	Ala	Pro	Glu
465					470					475					480
Gln	Trp	Gly	Met	Pro	Leu	Pro	Leu	Thr	Gln	Ser	Ser	Lys	Pro	Val	Ile
			485						490					495	
Asn	Ala	Glu	His	Asp	Gly	Arg	His	Trp	Arg	Arg	Ile	Pro	Glu	Pro	Met
		500						505					510		
Arg	Leu	Leu	Asp	Asp	Ala	Val	Glu	Arg	Ser	Ser					
		515					520								

<210> 330
 <211> 62
 <212> PRT
 <213> E. Coli

<400> 330
 Met Thr Ile Ser Asp Ile Ile Glu Ile Ile Val Val Cys Ala Leu Ile
 1 5 10 15
 Phe Phe Pro Leu Gly Tyr Leu Ala Arg His Ser Leu Arg Arg Ile Arg
 20 25 30
 Asp Thr Leu Arg Leu Phe Phe Ala Lys Pro Arg Tyr Val Lys Pro Ala
 35 40 45
 Gly Thr Leu Arg Arg Thr Glu Lys Ala Arg Ala Thr Lys Lys
 50 55 60

<210> 331
 <211> 559
 <212> PRT
 <213> E. Coli

<400> 331
 Met Thr Gln Phe Thr Gln Asn Thr Ala Met Pro Ser Ser Leu Trp Gln
 1 5 10 15
 Tyr Trp Arg Gly Leu Ser Gly Trp Asn Phe Tyr Phe Leu Val Lys Phe
 20 25 30
 Gly Leu Leu Trp Ala Gly Tyr Leu Asn Phe His Pro Leu Leu Asn Leu
 35 40 45
 Val Phe Ala Ala Phe Leu Leu Met Pro Leu Pro Arg Tyr Ser Leu His
 50 55 60
 Arg Leu Arg His Trp Ile Ala Leu Pro Ile Gly Phe Ala Leu Phe Trp
 65 70 75 80
 His Asp Thr Trp Leu Pro Gly Pro Glu Ser Ile Met Ser Gln Gly Ser
 85 90 95
 Gln Val Ala Gly Phe Ser Thr Asp Tyr Leu Ile Asp Leu Val Thr Arg
 100 105 110
 Phe Ile Asn Trp Gln Met Ile Gly Ala Ile Phe Val Leu Leu Val Ala
 115 120 125
 Trp Leu Phe Leu Ser Gln Trp Ile Arg Ile Thr Val Phe Val Val Ala
 130 135 140
 Ile Leu Leu Trp Leu Asn Val Leu Thr Leu Ala Gly Pro Ser Phe Ser
 145 150 155 160
 Leu Trp Pro Ala Gly Gln Pro Thr Thr Thr Val Thr Thr Thr Gly Gly
 165 170 175
 Asn Ala Ala Ala Thr Val Ala Ala Thr Gly Gly Ala Pro Val Val Gly
 180 185 190
 Asp Met Pro Ala Gln Thr Ala Pro Pro Thr Thr Ala Asn Leu Asn Ala
 195 200 205
 Trp Leu Asn Asn Phe Tyr Asn Ala Glu Ala Lys Arg Lys Ser Thr Phe
 210 215 220
 Pro Ser Ser Leu Pro Ala Asp Ala Gln Pro Phe Glu Leu Leu Val Ile
 225 230 235 240
 Asn Ile Cys Ser Leu Ser Trp Ser Asp Ile Glu Ala Ala Gly Leu Met
 245 250 255
 Ser His Pro Leu Trp Ser His Phe Asp Ile Glu Phe Lys Asn Phe Asn
 260 265 270

Ser	Ala	Thr	Ser	Tyr	Ser	Gly	Pro	Ala	Ala	Ile	Arg	Leu	Leu	Arg	Ala
		275					280					285			
Ser	Cys	Gly	Gln	Thr	Ser	His	Thr	Asn	Leu	Tyr	Gln	Pro	Ala	Asn	Asn
	290					295					300				
Asp	Cys	Tyr	Leu	Phe	Asp	Asn	Leu	Ser	Lys	Leu	Gly	Phe	Thr	Gln	His
305					310					315					320
Leu	Met	Met	Gly	His	Asn	Gly	Gln	Phe	Gly	Gly	Phe	Leu	Lys	Glu	Val
			325						330					335	
Arg	Glu	Asn	Gly	Gly	Met	Gln	Ser	Glu	Leu	Met	Asp	Gln	Thr	Asn	Leu
		340						345						350	
Pro	Val	Ile	Leu	Leu	Gly	Phe	Asp	Gly	Ser	Pro	Val	Tyr	Asp	Asp	Thr
		355					360						365		
Ala	Val	Leu	Asn	Arg	Trp	Leu	Asp	Val	Thr	Glu	Lys	Asp	Lys	Asn	Ser
	370					375					380				
Arg	Ser	Ala	Thr	Phe	Tyr	Asn	Thr	Leu	Pro	Leu	His	Asp	Gly	Asn	His
385					390					395					400
Tyr	Pro	Gly	Val	Ser	Lys	Thr	Ala	Asp	Tyr	Lys	Ala	Arg	Ala	Gln	Lys
			405						410					415	
Phe	Phe	Asp	Glu	Leu	Asp	Ala	Phe	Phe	Thr	Glu	Leu	Glu	Lys	Ser	Gly
		420					425						430		
Arg	Lys	Val	Met	Val	Val	Val	Val	Pro	Glu	His	Gly	Gly	Ala	Leu	Lys
	435						440						445		
Gly	Asp	Arg	Met	Gln	Val	Ser	Gly	Leu	Arg	Asp	Ile	Pro	Ser	Pro	Ser
	450					455					460				
Ile	Thr	Asp	Val	Pro	Val	Gly	Val	Lys	Phe	Phe	Gly	Met	Lys	Ala	Pro
465					470					475					480
His	Gln	Gly	Ala	Pro	Ile	Val	Ile	Glu	Gln	Pro	Ser	Ser	Phe	Leu	Ala
			485						490					495	
Ile	Ser	Asp	Leu	Val	Val	Arg	Val	Leu	Asp	Gly	Lys	Ile	Phe	Thr	Glu
		500						505					510		
Asp	Asn	Val	Asp	Trp	Lys	Lys	Leu	Thr	Ser	Gly	Leu	Pro	Gln	Thr	Ala
		515					520						525		
Pro	Val	Ser	Glu	Asn	Ser	Asn	Ala	Val	Val	Ile	Gln	Tyr	Gln	Asp	Lys
	530					535					540				
Pro	Tyr	Val	Arg	Leu	Asn	Gly	Gly	Asp	Trp	Val	Pro	Tyr	Pro	Gln	
545					550					555					

<210> 332
 <211> 127
 <212> PRT
 <213> E. Coli

<400> 332															
Met	Glu	Gly	Ser	Arg	Met	Lys	Tyr	Arg	Ile	Ala	Leu	Ala	Val	Ser	Leu
1				5					10					15	
Phe	Ala	Leu	Ser	Ala	Gly	Ser	Tyr	Ala	Thr	Thr	Leu	Cys	Gln	Glu	Lys
			20					25					30		
Glu	Gln	Asn	Ile	Leu	Lys	Glu	Ile	Ser	Tyr	Ala	Glu	Lys	His	Gln	Asn
		35					40					45			
Gln	Asn	Arg	Ile	Asp	Gly	Leu	Asn	Lys	Ala	Leu	Ser	Glu	Val	Arg	Ala
	50					55					60				
Asn	Cys	Ser	Asp	Ser	Gln	Leu	Arg	Ala	Asp	His	Gln	Lys	Lys	Ile	Ala
65					70					75					80
Lys	Gln	Lys	Asp	Glu	Val	Ala	Glu	Arg	Gln	Gln	Asp	Leu	Ala	Glu	Ala
			85						90					95	
Lys	Gln	Lys	Gly	Asp	Ala	Asp	Lys	Ile	Ala	Lys	Arg	Glu	Arg	Lys	Leu

	100		105		110
Ala	Glu	Ala	Gln	Glu	Glu
	115		120		125

<210> 333
 <211> 101
 <212> PRT
 <213> E. Coli

<400> 333

Met	Ser	Lys	Glu	His	Thr	Thr	Glu	His	Leu	Arg	Ala	Glu	Leu	Lys	Ser
1				5					10					15	
Leu	Ser	Asp	Thr	Leu	Glu	Glu	Val	Leu	Ser	Ser	Ser	Gly	Glu	Lys	Ser
			20					25					30		
Lys	Glu	Glu	Leu	Ser	Lys	Ile	Arg	Ser	Lys	Ala	Glu	Gln	Ala	Leu	Lys
			35				40					45			
Gln	Ser	Arg	Tyr	Arg	Leu	Gly	Glu	Thr	Gly	Asp	Ala	Ile	Ala	Lys	Gln
			50			55				60					
Thr	Arg	Val	Ala	Ala	Ala	Arg	Ala	Asp	Glu	Tyr	Val	Arg	Glu	Asn	Pro
65					70				75					80	
Trp	Thr	Gly	Val	Gly	Ile	Gly	Ala	Ala	Ile	Gly	Val	Val	Leu	Gly	Val
				85					90					95	
Leu	Leu	Ser	Arg	Arg											
				100											

<210> 334
 <211> 134
 <212> PRT
 <213> E. Coli

<400> 334

Met	Ala	Asp	Thr	His	His	Ala	Gln	Gly	Pro	Gly	Lys	Ser	Val	Leu	Gly
1				5					10					15	
Ile	Gly	Gln	Arg	Ile	Val	Ser	Ile	Met	Val	Glu	Met	Val	Glu	Thr	Arg
			20					25					30		
Leu	Arg	Leu	Ala	Val	Val	Glu	Leu	Glu	Glu	Glu	Lys	Ala	Asn	Leu	Phe
			35				40					45			
Gln	Leu	Leu	Leu	Met	Leu	Gly	Leu	Thr	Met	Leu	Phe	Ala	Ala	Phe	Gly
			50			55				60					
Leu	Met	Ser	Leu	Met	Val	Leu	Ile	Ile	Trp	Ala	Val	Asp	Pro	Gln	Tyr
65					70				75					80	
Arg	Leu	Asn	Ala	Met	Ile	Ala	Thr	Thr	Val	Val	Leu	Leu	Leu	Leu	Ala
				85					90					95	
Leu	Ile	Gly	Gly	Ile	Trp	Thr	Leu	Arg	Lys	Ser	Arg	Lys	Ser	Thr	Leu
			100					105					110		
Leu	Arg	His	Thr	Arg	His	Glu	Leu	Ala	Asn	Asp	Arg	Gln	Leu	Leu	Glu
			115				120					125			
Glu	Glu	Ser	Arg	Glu	Gln										
				130											

<210> 335
 <211> 99
 <212> PRT

<213> E. Coli

<400> 335

Met Ser Ser Lys Val Glu Arg Glu Arg Arg Lys Ala Gln Leu Leu Ser
1 5 10 15
Gln Ile Gln Gln Arg Leu Asp Leu Ser Ala Ser Arg Arg Glu Trp
20 25 30
Leu Glu Thr Thr Gly Ala Tyr Asp Arg Arg Trp Asn Met Leu Leu Ser
35 40 45
Leu Arg Ser Trp Ala Leu Val Gly Ser Ser Val Met Ala Ile Trp Thr
50 55 60
Ile Arg His Pro Asn Met Leu Val Arg Trp Ala Arg Arg Gly Phe Gly
65 70 75 80
Val Trp Ser Ala Trp Arg Leu Val Lys Thr Thr Leu Lys Gln Gln Gln
85 90 95
Leu Arg Gly

<210> 336

<211> 160

<212> PRT

<213> E. Coli

<400> 336

Met Ile Leu Ser Ile Asp Ser Asn Asp Ala Asn Thr Ala Pro Leu His
1 5 10 15
Lys Lys Thr Ile Ser Ser Leu Ser Gly Ala Val Glu Ser Met Met Lys
20 25 30
Lys Leu Glu Asp Val Gly Val Leu Val Ala Arg Ile Leu Met Pro Ile
35 40 45
Leu Phe Ile Thr Ala Gly Trp Gly Lys Ile Thr Gly Tyr Ala Gly Thr
50 55 60
Gln Gln Tyr Met Glu Ala Met Gly Val Pro Gly Phe Met Leu Pro Leu
65 70 75 80
Val Ile Leu Leu Glu Phe Gly Gly Gly Leu Ala Ile Leu Phe Gly Phe
85 90 95
Leu Thr Arg Thr Thr Ala Leu Phe Thr Ala Gly Phe Thr Leu Leu Thr
100 105 110
Ala Phe Leu Phe His Ser Asn Phe Ala Glu Gly Val Asn Ser Leu Met
115 120 125
Phe Met Lys Asn Leu Thr Ile Ser Gly Gly Phe Leu Leu Leu Ala Ile
130 135 140
Thr Gly Pro Gly Ala Tyr Ser Ile Asp Arg Leu Leu Asn Lys Lys Trp
145 150 155 160

<210> 337

<211> 296

<212> PRT

<213> E. Coli

<400> 337

Met Ile Lys Lys Thr Thr Glu Ile Asp Ala Ile Leu Leu Asn Leu Asn
1 5 10 15

Lys	Ala	Ile	Asp	Ala	His	Tyr	Gln	Trp	Leu	Val	Ser	Met	Phe	His	Ser
			20					25					30		
Val	Val	Ala	Arg	Asp	Ala	Ser	Lys	Pro	Glu	Ile	Thr	Asp	Asn	His	Ser
		35					40					45			
Tyr	Gly	Leu	Cys	Gln	Phe	Gly	Arg	Trp	Ile	Asp	His	Leu	Gly	Pro	Leu
	50					55					60				
Asp	Asn	Asp	Glu	Leu	Pro	Tyr	Val	Arg	Leu	Met	Asp	Ser	Ala	His	Gln
65					70					75					80
His	Met	His	Asn	Cys	Gly	Arg	Glu	Leu	Met	Leu	Ala	Ile	Val	Glu	Asn
			85						90					95	
His	Trp	Gln	Asp	Ala	His	Phe	Asp	Ala	Phe	Gln	Glu	Gly	Leu	Leu	Ser
			100					105					110		
Phe	Thr	Ala	Ala	Leu	Thr	Asp	Tyr	Lys	Ile	Tyr	Leu	Leu	Thr	Ile	Arg
		115					120					125			
Ser	Asn	Met	Asp	Val	Leu	Thr	Gly	Leu	Pro	Gly	Arg	Arg	Val	Leu	Asp
	130					135					140				
Glu	Ser	Phe	Asp	His	Gln	Leu	Arg	Asn	Ala	Glu	Pro	Leu	Asn	Leu	Tyr
145					150					155					160
Leu	Met	Leu	Leu	Asp	Ile	Asp	Arg	Phe	Lys	Leu	Val	Asn	Asp	Thr	Tyr
				165					170					175	
Gly	His	Leu	Ile	Gly	Asp	Val	Val	Leu	Arg	Thr	Leu	Ala	Thr	Tyr	Leu
			180					185					190		
Ala	Ser	Trp	Thr	Arg	Asp	Tyr	Glu	Thr	Val	Tyr	Arg	Tyr	Gly	Gly	Glu
		195					200					205			
Glu	Phe	Ile	Ile	Ile	Val	Lys	Ala	Ala	Asn	Asp	Glu	Glu	Ala	Cys	Arg
	210					215					220				
Ala	Gly	Val	Arg	Ile	Cys	Gln	Leu	Val	Asp	Asn	His	Ala	Ile	Thr	His
225					230					235					240
Ser	Glu	Gly	His	Ile	Asn	Ile	Thr	Val	Thr	Ala	Gly	Val	Ser	Arg	Ala
				245					250					255	
Phe	Pro	Glu	Glu	Pro	Leu	Asp	Val	Val	Ile	Gly	Arg	Ala	Asp	Arg	Ala
			260					265					270		
Met	Tyr	Glu	Gly	Lys	Gln	Thr	Gly	Arg	Asn	Arg	Cys	Met	Phe	Ile	Asp
		275					280					285			
Glu	Gln	Asn	Val	Ile	Asn	Arg	Val								
	290					295									

<210> 338
 <211> 203
 <212> PRT
 <213> E. Coli

<400> 338															
Met	Arg	Leu	Arg	Val	Val	Pro	Gly	Phe	Ile	Ser	Pro	Pro	Pro	Gly	Phe
1				5					10					15	
Gly	Gly	Leu	Gly	Tyr	Thr	Pro	Thr	Ala	Arg	Ala	Cys	Val	Asn	Ile	Ser
			20					25					30		
Ile	Pro	Leu	Gln	Leu	Arg	Val	Ile	Asp	Met	Leu	Asp	Val	Phe	Thr	Pro
		35					40					45			
Leu	Leu	Lys	Leu	Phe	Ala	Asn	Glu	Pro	Leu	Glu	Arg	Leu	Met	Tyr	Thr
	50					55					60				
Ile	Ile	Ile	Phe	Gly	Leu	Thr	Leu	Trp	Leu	Ile	Pro	Lys	Glu	Phe	Thr
65					70					75					80
Val	Ala	Phe	Asn	Ala	Tyr	Thr	Glu	Ile	Pro	Trp	Leu	Phe	Gln	Ile	Ile
				85					90					95	

Gly	Lys	Ala	Ala	Gln	Pro	Asp	Gly	His	Thr	Leu	Ala	Arg	Leu	Trp	Gly	145	150	155	160
Ala	Leu	Pro	Pro	Asp	Ile	Arg	Leu	Ser	Pro	His	Leu	Tyr	Leu	Ala	Thr	165	170	175	
Asn	Ser	Ala	Gln	Gly	Pro	Trp	Trp	Ile	Leu	Gly	Trp	Ser	Glu	Arg	Val	180	185	190	
Pro	Gly	Ala	Glu	Asp	Val	Leu	Pro	Ala	Pro	Leu	Pro	Pro	Tyr	Arg	Val	195	200	205	
Leu	Thr	Gly	Met	Ala	Asp	Arg	Phe	Gly	Arg	Thr	Leu	Thr	Tyr	Arg	Arg	210	215	220	
Glu	Ala	Ala	Gly	Asp	Leu	Ala	Gly	Glu	Ile	Thr	Gly	Val	Thr	Asp	Gly	225	230	235	240
Ala	Gly	Arg	Glu	Phe	Arg	Leu	Val	Leu	Thr	Thr	Gln	Ala	Gln	Arg	Ala	245	250	255	
Glu	Glu	Ala	Arg	Thr	Ser	Ser	Leu	Ser	Ser	Ser	Asp	Ser	Ser	Arg	Pro	260	265	270	
Leu	Ser	Ala	Ser	Ala	Phe	Pro	Asp	Thr	Leu	Pro	Gly	Thr	Glu	Tyr	Gly	275	280	285	
Pro	Asp	Arg	Gly	Ile	Arg	Leu	Ser	Ala	Val	Trp	Leu	Met	His	Asp	Pro	290	295	300	
Ala	Tyr	Pro	Glu	Ser	Leu	Pro	Ala	Ala	Pro	Leu	Val	Arg	Tyr	Thr	Tyr	305	310	315	320
Thr	Glu	Ala	Gly	Glu	Leu	Leu	Ala	Val	Tyr	Asp	Arg	Ser	Asn	Thr	Gln	325	330	335	
Val	Arg	Ala	Phe	Thr	Tyr	Asp	Ala	Gln	His	Pro	Gly	Arg	Met	Val	Ala	340	345	350	
His	Arg	Tyr	Ala	Gly	Arg	Pro	Glu	Met	Arg	Tyr	Arg	Tyr	Asp	Asp	Thr	355	360	365	
Gly	Arg	Val	Val	Glu	Gln	Leu	Asn	Pro	Ala	Gly	Leu	Ser	Tyr	Arg	Tyr	370	375	380	
Leu	Tyr	Glu	Gln	Asp	Arg	Ile	Thr	Val	Thr	Asp	Ser	Leu	Asn	Arg	Arg	385	390	395	400
Glu	Val	Leu	His	Thr	Glu	Gly	Gly	Ala	Gly	Leu	Lys	Arg	Val	Val	Lys	405	410	415	
Lys	Glu	Leu	Ala	Asp	Gly	Ser	Val	Thr	Arg	Ser	Gly	Tyr	Asp	Ala	Ala	420	425	430	
Gly	Arg	Leu	Thr	Ala	Gln	Thr	Asp	Ala	Ala	Gly	Arg	Arg	Thr	Glu	Tyr	435	440	445	
Gly	Leu	Asn	Val	Val	Ser	Gly	Asp	Ile	Thr	Asp	Ile	Thr	Thr	Pro	Asp	450	455	460	
Gly	Arg	Glu	Thr	Lys	Phe	Tyr	Tyr	Asn	Asp	Gly	Asn	Gln	Leu	Thr	Ala	465	470	475	480
Val	Val	Ser	Pro	Asp	Gly	Leu	Glu	Ser	Arg	Arg	Glu	Tyr	Asp	Glu	Pro	485	490	495	
Gly	Arg	Leu	Val	Ser	Glu	Thr	Ser	Arg	Ser	Gly	Glu	Thr	Val	Arg	Tyr	500	505	510	
Arg	Tyr	Asp	Asp	Ala	His	Ser	Glu	Leu	Pro	Ala	Thr	Thr	Thr	Asp	Ala	515	520	525	
Thr	Gly	Ser	Thr	Arg	Gln	Met	Thr	Trp	Ser	Arg	Tyr	Gly	Gln	Leu	Leu	530	535	540	
Ala	Phe	Thr	Asp	Cys	Ser	Gly	Tyr	Gln	Thr	Arg	Tyr	Glu	Tyr	Asp	Arg	545	550	555	560
Phe	Gly	Gln	Met	Thr	Ala	Val	His	Arg	Glu	Glu	Gly	Ile	Ser	Leu	Tyr	565	570	575	
Arg	Arg	Tyr	Asp	Asn	Arg	Gly	Arg	Leu	Thr	Ser	Val	Lys	Asp	Ala	Gln	580	585	590	
Gly	Arg	Glu	Thr	Arg	Tyr	Glu	Tyr	Asn	Ala	Ala	Gly	Asp	Leu	Thr	Ala				

Val	Ile	Thr	Pro	Asp	Gly	Asn	Arg	Ser	Glu	Thr	Gln	Tyr	Asp	Ala	Trp
610						615					620				
Gly	Lys	Ala	Val	Ser	Thr	Thr	Gln	Gly	Gly	Leu	Thr	Arg	Ser	Met	Glu
625					630					635					640
Tyr	Asp	Ala	Ala	Gly	Arg	Val	Ile	Ser	Leu	Thr	Asn	Glu	Asn	Gly	Ser
				645					650					655	
His	Ser	Val	Phe	Ser	Tyr	Asp	Ala	Leu	Asp	Arg	Leu	Val	Gln	Gln	Gly
			660					665					670		
Gly	Phe	Asp	Gly	Arg	Thr	Gln	Arg	Tyr	His	Tyr	Asp	Leu	Thr	Gly	Lys
		675				680						685			
Leu	Thr	Gln	Ser	Glu	Asp	Glu	Gly	Leu	Val	Ile	Leu	Trp	Tyr	Tyr	Asp
	690					695					700				
Glu	Ser	Asp	Arg	Ile	Thr	His	Arg	Thr	Val	Asn	Gly	Glu	Pro	Ala	Glu
705					710					715					720
Gln	Trp	Gln	Tyr	Asp	Gly	His	Gly	Trp	Leu	Thr	Asp	Ile	Ser	His	Leu
				725					730					735	
Ser	Glu	Gly	His	Arg	Val	Ala	Val	His	Tyr	Gly	Tyr	Asp	Asp	Lys	Gly
			740					745					750		
Arg	Leu	Thr	Gly	Glu	Cys	Gln	Thr	Val	Glu	Asn	Pro	Glu	Thr	Gly	Glu
		755				760						765			
Leu	Leu	Trp	Gln	His	Glu	Thr	Lys	His	Ala	Tyr	Asn	Glu	Gln	Gly	Leu
	770					775					780				
Ala	Asn	Arg	Val	Thr	Pro	Asp	Ser	Leu	Pro	Pro	Val	Glu	Trp	Leu	Thr
785					790					795					800
Tyr	Gly	Ser	Gly	Tyr	Leu	Ala	Gly	Met	Lys	Leu	Gly	Gly	Thr	Pro	Leu
				805					810					815	
Val	Glu	Tyr	Thr	Arg	Asp	Arg	Leu	His	Arg	Glu	Thr	Val	Arg	Ser	Phe
			820					825					830		
Gly	Ser	Met	Ala	Gly	Ser	Asn	Ala	Ala	Tyr	Glu	Leu	Thr	Ser	Thr	Tyr
		835				840						845			
Thr	Pro	Ala	Gly	Gln	Leu	Gln	Ser	Gln	His	Leu	Asn	Ser	Leu	Val	Tyr
	850					855					860				
Asp	Arg	Asp	Tyr	Gly	Trp	Ser	Asp	Asn	Gly	Asp	Leu	Val	Arg	Ile	Ser
865				870						875					880
Gly	Pro	Arg	Gln	Thr	Arg	Glu	Tyr	Gly	Tyr	Ser	Ala	Thr	Gly	Arg	Leu
				885					890					895	
Glu	Ser	Val	Arg	Thr	Leu	Ala	Pro	Asp	Leu	Asp	Ile	Arg	Ile	Pro	Tyr
			900					905					910		
Ala	Thr	Asp	Pro	Ala	Gly	Asn	Arg	Leu	Pro	Asp	Pro	Glu	Leu	His	Pro
	915						920					925			
Asp	Ser	Thr	Leu	Thr	Val	Trp	Pro	Asp	Asn	Arg	Ile	Ala	Glu	Asp	Ala
	930					935					940				
His	Tyr	Val	Tyr	Arg	His	Asp	Glu	Tyr	Gly	Arg	Leu	Thr	Glu	Lys	Thr
945					950					955					960
Asp	Arg	Ile	Pro	Ala	Gly	Val	Ile	Arg	Thr	Asp	Asp	Glu	Arg	Thr	His
				965					970					975	
His	Tyr	His	Tyr	Asp	Ser	Gln	His	Arg	Leu	Val	Phe	Tyr	Thr	Arg	Ile
			980					985					990		
Gln	His	Gly	Glu	Pro	Leu	Val	Glu	Ser	Arg	Tyr	Leu	Tyr	Asp	Pro	Leu
	995						1000					1005			
Gly	Arg	Arg	Met	Ala	Lys	Arg	Val	Trp	Arg	Arg	Glu	Arg	Asp	Leu	Thr
	1010					1015					1020				
Gly	Trp	Met	Ser	Leu	Ser	Arg	Lys	Pro	Glu	Val	Thr	Trp	Tyr	Gly	Trp
1025					1030					1035					1040
Asp	Gly	Asp	Arg	Leu	Thr	Thr	Val	Gln	Thr	Asp	Thr	Thr	Arg	Ile	Gln
				1045					1050					1055	

Thr Val Tyr Glu Pro Gly Ser Phe Thr Pro Leu Ile Arg Val Glu Thr
 1060 1065 1070
 Glu Asn Gly Glu Arg Glu Lys Ala Gln Arg Arg Ser Leu Ala Glu Thr
 1075 1080 1085
 Leu Gln Gln Glu Gly Ser Glu Asn Gly His Gly Val Val Phe Pro Ala
 1090 1095 1100
 Glu Leu Val Arg Leu Leu Asp Arg Leu Glu Glu Ile Arg Ala Asp
 1105 1110 1115 1120
 Arg Val Ser Ser Glu Ser Arg Ala Trp Leu Ala Gln Cys Gly Leu Thr
 1125 1130 1135
 Val Glu Gln Leu Ala Arg Gln Val Glu Pro Glu Tyr Thr Pro Ala Arg
 1140 1145 1150
 Lys Ala His Leu Tyr His Cys Asp His Arg Gly Leu Pro Leu Ala Leu
 1155 1160 1165
 Ile Ser Glu Asp Gly Asn Thr Ala Trp Ser Ala Glu Tyr Asp Glu Trp
 1170 1175 1180
 Gly Asn Gln Leu Asn Glu Glu Asn Pro His His Val Tyr Gln Pro Tyr
 1185 1190 1195 1200
 Arg Leu Pro Gly Gln Gln His Asp Glu Glu Ser Gly Leu Tyr Tyr Asn
 1205 1210 1215
 Arg His Arg Tyr Tyr Asp Pro Leu Gln Gly Arg Tyr Ile Thr Gln Asp
 1220 1225 1230
 Pro Met Gly Leu Lys Gly Gly Trp Asn Leu Tyr Gln Tyr Pro Leu Asn
 1235 1240 1245
 Pro Leu Gln Gln Ile Asp Pro Met Gly Leu Leu Gln Thr Trp Asp Asp
 1250 1255 1260
 Ala Arg Ser Gly Ala Cys Thr Gly Gly Val Cys Gly Val Leu Ser Arg
 1265 1270 1275 1280
 Ile Ile Gly Pro Ser Lys Phe Asp Ser Thr Ala Asp Ala Ala Leu Asp
 1285 1290 1295
 Ala Leu Lys Glu Thr Gln Asn Arg Ser Leu Cys Asn Asp Met Glu Tyr
 1300 1305 1310
 Ser Gly Ile Val Cys Lys Asp Thr Asn Gly Lys Tyr Phe Ala Ser Lys
 1315 1320 1325
 Ala Glu Thr Asp Asn Leu Arg Lys Glu Ser Tyr Pro Leu Lys Arg Lys
 1330 1335 1340
 Cys Pro Thr Gly Thr Asp Arg Val Ala Ala Tyr His Thr His Gly Ala
 1345 1350 1355 1360
 Asp Ser His Gly Asp Tyr Val Asp Glu Phe Phe Ser Ser Ser Asp Lys
 1365 1370 1375
 Asn Leu Val Arg Ser Lys Asp Asn Asn Leu Glu Ala Phe Tyr Leu Ala
 1380 1385 1390
 Thr Pro Asp Gly Arg Phe Glu Ala Leu Asn Asn Lys Gly Glu Tyr Ile
 1395 1400 1405
 Phe Ile Arg Asn Ser Val Pro Gly Leu Ser Ser Val Cys Ile Pro Tyr
 1410 1415 1420
 His Asp
 1425

<210> 341
 <211> 122
 <212> PRT
 <213> E. Coli

<400> 341
 Met Lys Tyr Ser Ser Ile Phe Ser Met Leu Ser Phe Phe Ile Leu Phe

<212> PRT
<213> E. Coli

<400> 343

Met	Leu	Ala	Ile	Ser	Ser	Asn	Leu	Ser	Lys	Met	Ile	Ile	Phe	Ile	Phe
1				5					10					15	
Ala	Ile	Ile	Ile	Ile	Val	Val	Leu	Cys	Val	Ile	Thr	Tyr	Leu	Tyr	Leu
			20					25					30		
Tyr	Lys	Asp	Glu	Ser	Leu	Val	Ser	Lys	His	Tyr	Ile	Asn	Tyr	Met	Ala
		35					40					45			
Ile	Pro	Glu	Asn	Asp	Gly	Val	Phe	Thr	Trp	Leu	Pro	Asp	Phe	Phe	Pro
	50					55					60				
His	Val	Ala	Val	Asp	Ile	Ser	Ile	Tyr	Thr	Asn	Val	Glu	Asp	Asp	Tyr
65					70					75					80
Phe	Phe	Leu	Ile	Phe	Pro										
					85										

<210> 344
<211> 63
<212> PRT
<213> E. Coli

<400> 344

Met	Arg	Ala	Arg	Glu	Gln	Val	Ala	Lys	Ile	Val	Ser	Lys	Asn	Asp	Pro
1				5					10					15	
Asp	Thr	Lys	Lys	Val	Trp	Cys	Lys	Tyr	Gly	Lys	Ile	Pro	Gly	Gln	Gly
			20					25					30		
Asp	Gly	Val	Asn	Leu	Phe	Phe	Val	Gly	Glu	Ile	Asn	Val	Thr	His	Tyr
		35					40					45			
Phe	Ile	Thr	Asn	Ile	Gly	Ala	Gly	Leu	Pro	Asp	Ala	Cys	Ala	Glu	
	50					55					60				

<210> 345
<211> 167
<212> PRT
<213> E. Coli

<400> 345

Met	Pro	Gly	Asn	Ser	Pro	His	Tyr	Gly	Arg	Trp	Pro	Gln	His	Asp	Phe
1				5					10					15	
Thr	Ser	Leu	Lys	Leu	Arg	Pro	Gln	Ser	Val	Thr	Ser	Arg	Ile	Gln	
		20					25					30			
Pro	Gly	Ser	Asp	Val	Ile	Val	Cys	Ala	Glu	Met	Asp	Glu	Gln	Trp	Gly
		35					40					45			
Tyr	Val	Gly	Ala	Lys	Ser	Arg	Gln	Arg	Trp	Leu	Phe	Tyr	Ala	Tyr	Asp
	50					55					60				
Ser	Leu	Arg	Lys	Thr	Val	Val	Ala	His	Val	Phe	Gly	Glu	Arg	Thr	Met
65					70					75					80
Ala	Thr	Leu	Gly	Arg	Leu	Met	Ser	Leu	Leu	Ser	Pro	Phe	Asp	Val	Val
				85					90					95	
Ile	Trp	Met	Thr	Asp	Gly	Trp	Pro	Leu	Tyr	Glu	Ser	Arg	Leu	Lys	Gly
		100						105					110		
Lys	Leu	His	Val	Ile	Ser	Lys	Arg	Tyr	Thr	Gln	Arg	Ile	Glu	Arg	His

	115		120		125										
Asn	Leu	Asn	Leu	Arg	Gln	His	Leu	Ala	Arg	Leu	Gly	Arg	Lys	Ser	Leu
	130					135					140				
Ser	Phe	Ser	Lys	Ser	Val	Glu	Leu	His	Asp	Lys	Val	Ile	Gly	His	Tyr
145					150					155					160
Leu	Asn	Ile	Lys	His	Tyr	Gln									
				165											

<210> 346
 <211> 91
 <212> PRT
 <213> E. Coli

	<400>	346													
Met	Ala	Ser	Val	Ser	Ile	Ser	Cys	Pro	Ser	Cys	Ser	Ala	Thr	Asp	Gly
1				5					10					15	
Val	Val	Arg	Asn	Gly	Lys	Ser	Thr	Ala	Gly	His	Gln	Arg	Tyr	Leu	Cys
			20					25					30		
Ser	His	Cys	Arg	Lys	Thr	Trp	Gln	Leu	Gln	Phe	Thr	Tyr	Thr	Ala	Ser
		35					40					45			
Gln	Pro	Gly	Thr	His	Gln	Lys	Ile	Ile	Asp	Met	Ala	Met	Asn	Gly	Val
	50					55				60					
Gly	Cys	Arg	Ala	Thr	Ala	Arg	Ile	Met	Gly	Val	Gly	Leu	Asn	Thr	Ile
65					70					75					80
Leu	Arg	His	Leu	Lys	Asn	Ser	Gly	Arg	Ser	Arg					
				85					90						

<210> 347
 <211> 138
 <212> PRT
 <213> E. Coli

	<400>	347													
Met	Met	Thr	Lys	Thr	Gln	Ile	Asn	Lys	Leu	Ile	Lys	Met	Met	Asn	Asp
1				5					10					15	
Leu	Asp	Tyr	Pro	Phe	Glu	Ala	Pro	Leu	Lys	Glu	Ser	Phe	Ile	Glu	Ser
			20					25					30		
Ile	Ile	Gln	Ile	Glu	Phe	Asn	Ser	Asn	Ser	Thr	Asn	Cys	Leu	Glu	Lys
		35					40					45			
Leu	Cys	Asn	Glu	Val	Ser	Ile	Leu	Phe	Lys	Asn	Gln	Pro	Asp	Tyr	Leu
	50					55				60					
Thr	Phe	Leu	Arg	Ala	Met	Asp	Gly	Phe	Glu	Val	Asn	Gly	Leu	Arg	Leu
65					70					75					80
Phe	Ser	Leu	Ser	Ile	Pro	Glu	Pro	Ser	Val	Lys	Asn	Leu	Phe	Ala	Val
				85					90					95	
Asn	Glu	Phe	Tyr	Arg	Asn	Asn	Asp	Asp	Phe	Ile	Asn	Pro	Asp	Leu	Gln
			100				105						110		
Glu	Arg	Leu	Val	Ile	Gly	Asp	Tyr	Ser	Ile	Ser	Ile	Phe	Thr	Tyr	Asp
		115					120					125			
Ile	Lys	Gly	Asp	Ala	Ala	Asn	Leu	Leu	Ile						
	130					135									

<210> 348

<211> 392
 <212> PRT
 <213> E. Coli

<400> 348

Met	Ser	Asn	Ile	Val	Tyr	Leu	Thr	Val	Thr	Gly	Glu	Gln	Gln	Gly	Ser
1			5						10					15	
Ile	Ser	Ala	Gly	Cys	Gly	Thr	Ser	Glu	Ser	Thr	Gly	Asn	Arg	Trp	Gln
			20					25					30		
Ser	Gly	His	Glu	Asp	Glu	Ile	Phe	Thr	Phe	Ser	Leu	Leu	Asn	Asn	Ile
		35					40					45			
Asn	Asn	Thr	Gly	Leu	Gly	Ser	Gln	Phe	His	Gly	Ile	Thr	Phe	Cys	Lys
	50					55					60				
Leu	Ile	Asp	Lys	Ser	Thr	Pro	Leu	Phe	Ile	Asn	Ser	Ile	Asn	Asn	Asn
65					70					75					80
Glu	Gln	Leu	Phe	Met	Gly	Phe	Asp	Phe	Tyr	Arg	Ile	Asn	Arg	Phe	Gly
			85						90					95	
Arg	Leu	Glu	Lys	Tyr	Tyr	Tyr	Ile	Gln	Leu	Arg	Gly	Ala	Phe	Leu	Ser
			100					105					110		
Ala	Ile	His	His	Gln	Ile	Ile	Glu	Asn	Gln	Leu	Asp	Thr	Glu	Thr	Ile
		115					120					125			
Thr	Ile	Ser	Tyr	Glu	Phe	Ile	Leu	Cys	Gln	His	Leu	Ile	Ala	Asn	Thr
	130					135					140				
Glu	Phe	Ser	Tyr	Leu	Ala	Leu	Pro	Glu	Asn	Tyr	Asn	Arg	Leu	Phe	Leu
145					150					155					160
Pro	Asn	Ser	Lys	Asn	Gln	Thr	Asn	Asn	Arg	Phe	Lys	Thr	Leu	Asn	Ser
			165						170					175	
Lys	Ala	Ile	Gly	Arg	Leu	Leu	Ala	Ala	Gly	Gly	Val	Tyr	Asn	Gly	Asn
			180					185					190		
Ile	Glu	Gly	Phe	Arg	Asp	Thr	Ala	Glu	Lys	Leu	Gly	Gly	Asp	Ala	Ile
		195					200					205			
Lys	Gly	Tyr	Asp	Gln	Ile	Leu	Asn	Glu	Lys	Thr	Ala	Gly	Ile	Ala	Ile
	210					215					220				
Ala	Thr	Ala	Ser	Ile	Leu	Leu	Thr	Lys	Arg	Ser	Asn	Val	Asp	Thr	Tyr
225					230					235					240
Thr	Glu	Ile	Asn	Ser	Tyr	Leu	Gly	Lys	Leu	Arg	Gly	Gln	Gln	Lys	Leu
			245						250					255	
Leu	Asp	Gly	Ile	Asp	Ile	Ile	Glu	Ile	Ile	Tyr	Ile	Lys	Arg	Pro	Ser
		260					265						270		
Lys	Asp	Leu	Ala	Asn	Leu	Arg	Lys	Glu	Phe	Asn	Lys	Thr	Val	Arg	Lys
	275						280					285			
Asn	Phe	Leu	Ile	Lys	Leu	Ala	Lys	Thr	Ser	Glu	Ala	Ser	Gly	Arg	Phe
	290					295					300				
Asn	Ala	Glu	Asp	Leu	Leu	Arg	Met	Arg	Lys	Gly	Asn	Val	Pro	Leu	Asn
305					310					315					320
Tyr	Asn	Val	His	His	Lys	Leu	Ser	Leu	Asp	Asp	Gly	Gly	Thr	Asn	Asp
			325						330					335	
Phe	Glu	Asn	Leu	Val	Leu	Ile	Glu	Asn	Glu	Pro	Tyr	His	Lys	Val	Phe
		340						345					350		
Thr	Asn	Met	Gln	Ser	Arg	Ile	Ala	Lys	Gly	Ile	Leu	Val	Gly	Glu	Ser
	355						360						365		
Lys	Ile	Thr	Pro	Trp	Ala	Ile	Pro	Ser	Gly	Ser	Ile	Tyr	Pro	Pro	Met
	370					375					380				
Lys	Asn	Ile	Met	Asp	His	Thr	Lys								
385					390										

<210> 349
 <211> 221
 <212> PRT
 <213> E. Coli

<400> 349

Met	Val	Leu	Ala	Leu	Asn	Tyr	Asn	Met	His	Gly	Val	Asn	Ile	Arg	Ser
1				5					10					15	
Glu	Asn	Ala	Ala	Lys	Pro	His	Thr	Met	Pro	Ser	Arg	Tyr	Leu	Cys	Glu
			20					25					30		
Tyr	Ile	Arg	Ser	Ile	Glu	Lys	Asn	Gly	His	Ala	Leu	Asp	Phe	Gly	Cys
		35					40					45			
Gly	Lys	Leu	Arg	Tyr	Ser	Asp	Glu	Leu	Ile	Ser	Lys	Phe	Asp	Glu	Val
	50					55					60				
Thr	Phe	Leu	Asp	Ser	Lys	Arg	Gln	Leu	Glu	Arg	Glu	Gln	Ile	Ile	Arg
65					70					75					80
Gly	Ile	Lys	Thr	Lys	Ile	Ile	Asp	Tyr	Val	Pro	Arg	Tyr	Tyr	Lys	Asn
				85					90					95	
Ala	Asn	Thr	Val	Ala	Phe	Glu	Asp	Val	Asp	Lys	Ile	Ile	Gly	Gly	Tyr
			100					105					110		
Asp	Phe	Ile	Leu	Cys	Ser	Asn	Val	Leu	Ser	Ala	Val	Pro	Cys	Arg	Asp
	115					120						125			
Thr	Ile	Asp	Lys	Ile	Val	Leu	Ser	Ile	Lys	Arg	Leu	Leu	Lys	Ser	Gly
	130					135					140				
Gly	Glu	Thr	Leu	Ile	Val	Asn	Gln	Tyr	Lys	Ser	Ser	Tyr	Phe	Lys	Lys
145					150					155					160
Tyr	Glu	Thr	Gly	Arg	Lys	His	Leu	Tyr	Gly	Tyr	Ile	Tyr	Lys	Asn	Ser
				165					170					175	
Lys	Ser	Val	Ser	Tyr	Tyr	Gly	Leu	Leu	Asp	Glu	Leu	Ala	Val	Gln	Glu
			180					185					190		
Ile	Cys	Ser	Ser	His	Gly	Leu	Glu	Ile	Leu	Lys	Ser	Trp	Ser	Lys	Ala
	195					200						205			
Gly	Ser	Ser	Tyr	Val	Thr	Val	Gly	Ser	Cys	Asn	Ala	Ile			
	210					215					220				

<210> 350
 <211> 234
 <212> PRT
 <213> E. Coli

<400> 350

Met	Asn	Asn	Met	Phe	Glu	Pro	Pro	Lys	Asn	Tyr	Asn	Glu	Met	Leu	Pro
1				5					10					15	
Lys	Leu	His	Lys	Ala	Thr	Phe	Leu	Asn	Thr	Leu	Ile	Tyr	Cys	Ile	Leu
			20					25					30		
Leu	Val	Ile	Tyr	Glu	Tyr	Ile	Pro	Leu	Ile	Thr	Leu	Pro	Thr	Lys	Tyr
		35					40					45			
Val	Pro	Pro	Ile	Lys	Asp	His	Glu	Ser	Phe	Ile	Asn	Trp	Ala	Leu	Ser
	50					55					60				
Phe	Gly	Ile	Leu	Pro	Cys	Ala	Phe	Ala	Ile	Phe	Ala	Tyr	Leu	Ile	Ser
65					70					75					80
Gly	Ala	Leu	Asp	Leu	His	Asn	Asn	Ala	Ala	Lys	Leu	Leu	Arg	Val	Arg
				85					90					95	
Tyr	Leu	Trp	Asp	Lys	His	Leu	Ile	Ile	Lys	Pro	Leu	Ser	Arg	Arg	Ala
			100					105					110		

Gly	Val	Asn	Arg	Lys	Leu	Asn	Lys	Asp	Glu	Ala	His	Asn	Val	Met	Ser
	115						120					125			
Asn	Leu	Tyr	Tyr	Pro	Glu	Val	Arg	Lys	Ile	Glu	Asp	Lys	His	Tyr	Ile
	130						135				140				
Glu	Leu	Phe	Trp	Asn	Lys	Val	Tyr	Tyr	Phe	Trp	Ile	Phe	Phe	Glu	Phe
145					150					155					160
Ser	Ile	Ile	Ala	Leu	Ile	Ser	Phe	Leu	Ile	Ile	Phe	Phe	Cys	Lys	Gln
			165						170					175	
Met	Asp	Ile	Phe	His	Val	Glu	Gly	Ser	Leu	Leu	Ser	Leu	Phe	Phe	Phe
			180					185					190		
Val	Ile	Leu	Ser	Phe	Ser	Val	Ser	Gly	Ile	Ile	Phe	Ala	Leu	Thr	Val
		195					200					205			
Lys	Pro	Arg	Thr	Glu	Ser	Gln	Val	Gly	Lys	Ile	Pro	Asp	Asp	Lys	Ile
	210					215					220				
Lys	Glu	Phe	Phe	Thr	Lys	Asn	Asn	Ile	Asn						
225					230										

<210> 351
 <211> 94
 <212> PRT
 <213> E. Coli

<400> 351															
Met	Phe	Thr	Ile	Asn	Ala	Glu	Val	Arg	Lys	Glu	Gln	Gly	Lys	Gly	Ala
1				5					10					15	
Ser	Arg	Arg	Leu	Arg	Ala	Ala	Asn	Lys	Phe	Pro	Ala	Ile	Ile	Tyr	Gly
			20					25					30		
Gly	Lys	Glu	Ala	Pro	Leu	Ala	Ile	Glu	Leu	Asp	His	Asp	Lys	Val	Met
		35					40					45			
Asn	Met	Gln	Ala	Lys	Ala	Glu	Phe	Tyr	Ser	Glu	Val	Leu	Thr	Ile	Val
	50					55					60				
Val	Asp	Gly	Lys	Glu	Ile	Lys	Val	Lys	Ala	Gln	Asp	Val	Gln	Arg	His
65					70					75					80
Pro	Tyr	Lys	Pro	Lys	Leu	Gln	His	Ile	Asp	Phe	Val	Arg	Ala		
				85					90						

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 <211> 658
 <212> PRT
 <213> E. Coli

<400> 352															
Met	Val	Leu	Phe	Tyr	Arg	Ala	His	Trp	Arg	Asp	Tyr	Lys	Asn	Asp	Gln
1				5					10					15	
Val	Arg	Ile	Met	Met	Asn	Leu	Thr	Thr	Leu	Thr	His	Arg	Asp	Ala	Leu
			20					25					30		
Cys	Leu	Asn	Ala	Arg	Phe	Thr	Ser	Arg	Glu	Glu	Ala	Ile	His	Ala	Leu
		35					40					45			
Thr	Gln	Arg	Leu	Ala	Ala	Leu	Gly	Lys	Ile	Ser	Ser	Thr	Glu	Gln	Phe
	50					55					60				
Leu	Glu	Glu	Val	Tyr	Arg	Arg	Glu	Ser	Leu	Gly	Pro	Thr	Ala	Leu	Gly
65					70					75					80
Glu	Gly	Leu	Ala	Val	Pro	His	Gly	Lys	Thr	Ala	Ala	Val	Lys	Glu	Ala
				85					90					95	

Ala 100	Phe	Ala	Val	Ala	Thr	Leu	Ser	Glu	Pro	Leu	Gln	Trp	Glu	Gly	Val
Asp 115	Gly	Pro	Glu	Ala	Val	Asp	Leu	Val	Val	Leu	Leu	Ala	Ile	Pro	Pro
Asn 130	Glu	Ala	Gly	Thr	Thr	His	Met	Gln	Leu	Leu	Thr	Ala	Leu	Thr	Thr
Arg 145	Leu	Ala	Asp	Asp	Glu	Ile	Arg	Ala	Arg	Ile	Gln	Ser	Ala	Thr	Thr
Pro 165	Asp	Glu	Leu	Leu	Ser	Ala	Leu	Asp	Asp	Lys	Gly	Gly	Thr	Gln	Pro
Ser 180	Ala	Ser	Phe	Ser	Asn	Ala	Pro	Thr	Ile	Val	Cys	Val	Thr	Ala	Cys
Pro 195	Ala	Gly	Ile	Ala	His	Thr	Tyr	Met	Ala	Ala	Glu	Tyr	Leu	Glu	Lys
Ala 210	Gly	Arg	Lys	Leu	Gly	Val	Asn	Val	Tyr	Val	Glu	Lys	Gln	Gly	Ala
Asn 225	Gly	Ile	Glu	Gly	Arg	Leu	Thr	Ala	Asp	Gln	Leu	Asn	Ser	Ala	Thr
Ala 245	Cys	Ile	Phe	Ala	Ala	Glu	Val	Ala	Ile	Lys	Glu	Ser	Glu	Arg	Phe
Asn 260	Gly	Ile	Pro	Ala	Leu	Ser	Val	Pro	Val	Ala	Glu	Pro	Ile	Arg	His
Ala 275	Glu	Ala	Leu	Ile	Gln	Gln	Ala	Leu	Thr	Leu	Lys	Arg	Ser	Asp	Glu
Thr 290	Arg	Thr	Val	Gln	Gln	Asp	Thr	Gln	Pro	Val	Lys	Ser	Val	Lys	Thr
Glu 305	Leu	Lys	Gln	Ala	Leu	Leu	Ser	Gly	Ile	Ser	Phe	Ala	Val	Pro	Leu
Ile 325	Val	Ala	Gly	Gly	Thr	Val	Leu	Ala	Val	Ala	Val	Leu	Leu	Ser	Gln
Ile 340	Phe	Gly	Leu	Gln	Asp	Leu	Phe	Asn	Glu	Glu	Asn	Ser	Trp	Leu	Trp
Met 355	Tyr	Arg	Lys	Leu	Gly	Gly	Gly	Leu	Leu	Gly	Ile	Leu	Met	Val	Pro
Val 370	Leu	Ala	Ala	Tyr	Thr	Ala	Tyr	Ser	Leu	Ala	Asp	Lys	Pro	Ala	Leu
Ala 385	Pro	Gly	Phe	Ala	Ala	Gly	Leu	Ala	Ala	Asn	Met	Ile	Gly	Ser	Gly
Phe 405	Leu	Gly	Ala	Val	Val	Gly	Gly	Leu	Ile	Ala	Gly	Tyr	Leu	Met	Arg
Trp 420	Val	Lys	Asn	His	Leu	Arg	Leu	Ser	Ser	Lys	Phe	Asn	Gly	Phe	Leu
Thr 435	Phe	Tyr	Leu	Tyr	Pro	Val	Leu	Gly	Thr	Leu	Gly	Ala	Gly	Ser	Leu
Met 450	Leu	Phe	Val	Val	Gly	Glu	Pro	Val	Ala	Trp	Ile	Asn	Asn	Ser	Leu
Thr 465	Ala	Trp	Leu	Asn	Gly	Leu	Ser	Gly	Ser	Asn	Ala	Leu	Leu	Leu	Gly
Ala 485	Ile	Leu	Gly	Phe	Met	Cys	Ser	Phe	Asp	Leu	Gly	Gly	Pro	Val	Asn
Lys 500	Ala	Ala	Tyr	Ala	Phe	Cys	Leu	Gly	Ala	Met	Ala	Asn	Gly	Val	Tyr
Gly 515	Pro	Tyr	Ala	Ile	Phe	Ala	Ser	Val	Lys	Met	Val	Ser	Ala	Phe	Thr
Val 530	Thr	Ala	Ser	Thr	Met	Leu	Ala	Pro	Arg	Leu	Phe	Lys	Glu	Phe	Glu
Ile 550	Glu	Thr	Gly	Lys	Ser	Thr	Trp	Leu	Leu	Gly	Leu	Ala	Gly	Ile	Thr

Ile	Asp	Gly	Lys	Tyr	Met	Arg	Val	His	Arg	Thr	Ile	Gly	Ser	Thr	Arg		
		275					280					285					
Met	Asp	Ile	Lys	Ile	Ala	His	Ala	Arg	Ile	Glu	Asn	Lys	Ile	Val	Asn		
	290					295					300						
Leu	Leu	Glu	Pro	Leu	Ala	Thr	Leu	Ala	Trp	Thr	Leu	Gly	Phe	Glu	Tyr		
305					310					315					320		
His	His	Gly	Leu	Leu	Glu	Lys	Met	Trp	Lys	Glu	Ile	Leu	Lys	Asn	His		
			325						330					335			
Ala	His	Asp	Ser	Ile	Gly	Cys	Cys	Cys	Ser	Asp	Lys	Val	His	Arg	Glu		
			340					345					350				
Ile	Val	Ala	Arg	Phe	Glu	Leu	Ala	Glu	Asp	Met	Ala	Asp	Asn	Leu	Ile		
		355					360					365					
Arg	Phe	Tyr	Met	Arg	Lys	Ile	Ala	Asp	Asn	Met	Pro	Gln	Ser	Asp	Ala		
	370					375					380						
Asp	Lys	Leu	Val	Leu	Phe	Asn	Leu	Met	Pro	Trp	Pro	Arg	Glu	Glu	Val		
385					390					395					400		
Ile	Asn	Thr	Thr	Val	Arg	Leu	Arg	Ala	Ser	Gln	Phe	Asn	Leu	Arg	Asp		
				405						410				415			
Asp	Arg	Gly	Gln	Pro	Val	Pro	Tyr	Phe	Ile	Arg	His	Ala	Arg	Glu	Ile		
			420					425				430					
Asp	Pro	Gly	Leu	Ile	Asp	Arg	Gln	Ile	Val	His	Tyr	Gly	Asn	Tyr	Asp		
		435				440						445					
Pro	Phe	Met	Glu	Phe	Asp	Ile	Gln	Ile	Asn	Gln	Ile	Val	Pro	Ser	Met		
	450					455					460						
Gly	Tyr	Arg	Thr	Leu	Tyr	Ile	Glu	Ala	Asn	Gln	Pro	Gly	Asn	Val	Ile		
465					470					475					480		
Ala	Ala	Lys	Ser	Asp	Ala	Glu	Gly	Ile	Leu	Glu	Asn	Ala	Phe	Trp	Gln		
				485					490					495			
Ile	Ala	Leu	Asn	Glu	Asp	Gly	Ser	Leu	Gln	Leu	Val	Asp	Lys	Asp	Ser		
			500					505					510				
Gly	Val	Arg	Tyr	Asp	Arg	Val	Leu	Gln	Ile	Glu	Glu	Ser	Ser	Asp	Asp		
		515					520					525					
Gly	Asp	Glu	Tyr	Asp	Tyr	Ser	Pro	Ala	Lys	Glu	Glu	Trp	Val	Ile	Thr		
	530					535					540						
Ala	Ala	Asn	Ala	Lys	Pro	Gln	Cys	Asp	Ile	Ile	His	Glu	Ala	Trp	Gln		
545					550					555					560		
Ser	Arg	Ala	Val	Ile	Arg	Tyr	Asp	Met	Ala	Val	Pro	Leu	Asn	Leu	Ser		
				565					570					575			
Glu	Arg	Ser	Ala	Arg	Gln	Ser	Thr	Gly	Arg	Val	Gly	Val	Val	Leu	Val		
			580					585					590				
Val	Thr	Leu	Ser	His	Asn	Ser	Arg	Arg	Ile	Asp	Val	Asp	Ile	Asn	Leu		
		595					600					605					
Asp	Asn	Gln	Ala	Asp	Asp	His	Arg	Leu	Arg	Val	Leu	Val	Pro	Thr	Pro		
	610					615					620						
Phe	Asn	Thr	Asp	Ser	Val	Leu	Ala	Asp	Thr	Gln	Phe	Gly	Ser	Leu	Thr		
625					630					635					640		
Arg	Pro	Val	Asn	Asp	Ser	Ala	Met	Asn	Asn	Trp	Gln	Gln	Glu	Gly	Trp		
				645					650					655			
Lys	Glu	Ala	Pro	Val	Pro	Val	Trp	Asn	Met	Leu	Asn	Tyr	Val	Ala	Leu		
		660						665					670				
Gln	Glu	Gly	Arg	Asn	Gly	Met	Ala	Val	Phe	Ser	Glu	Gly	Leu	Arg	Glu		
		675					680					685					
Phe	Glu	Val	Ile	Gly	Glu	Glu	Lys	Lys	Thr	Phe	Ala	Ile	Thr	Leu	Leu		
	690					695					700						
Arg	Gly	Val	Gly	Leu	Leu	Gly	Lys	Glu	Asp	Leu	Leu	Leu	Arg	Pro	Gly		
705				710					715					720			
Arg	Pro	Ser	Gly	Ile	Lys	Met	Pro	Val	Pro	Asp	Ser	Gln	Leu	Arg	Gly		

				725					730				735				
Leu	Leu	Ser	Cys	Arg	Leu	Ser	Leu	Leu	Ser	Tyr	Thr	Gly	Thr	Pro	Thr		
			740					745					750				
Ala	Ala	Gly	Val	Ala	Gln	Gln	Ala	Arg	Ala	Trp	Leu	Thr	Pro	Val	Gln		
		755					760					765					
Cys	Tyr	Asn	Lys	Ile	Pro	Trp	Asp	Val	Met	Lys	Leu	Asn	Lys	Ala	Gly		
	770					775					780						
Phe	Asn	Val	Pro	Glu	Ser	Tyr	Ser	Leu	Leu	Lys	Met	Pro	Pro	Val	Gly		
785					790					795					800		
Cys	Leu	Ile	Ser	Ala	Leu	Lys	Lys	Ala	Glu	Asp	Arg	Gln	Glu	Val	Ile		
				805					810					815			
Leu	Arg	Leu	Phe	Asn	Pro	Ala	Glu	Ser	Ala	Thr	Cys	Asp	Ala	Thr	Val		
			820					825					830				
Ala	Phe	Ser	Arg	Glu	Val	Ile	Ser	Cys	Ser	Glu	Thr	Met	Met	Asp	Glu		
		835					840					845					
His	Ile	Thr	Thr	Glu	Glu	Asn	Gln	Gly	Ser	Asn	Leu	Ser	Gly	Pro	Phe		
	850					855					860						
Leu	Pro	Gly	Gln	Ser	Arg	Thr	Phe	Ser	Tyr	Arg	Leu	Ala					
865					870					875							

<210> 354
 <211> 523
 <212> PRT
 <213> E. Coli

				<400> 354													
Met	Met	Leu	Asp	Ile	Val	Glu	Leu	Ser	Arg	Leu	Gln	Phe	Ala	Leu	Thr		
1				5					10					15			
Ala	Met	Tyr	His	Phe	Leu	Phe	Val	Pro	Leu	Thr	Leu	Gly	Met	Ala	Phe		
			20					25					30				
Leu	Leu	Ala	Ile	Met	Glu	Thr	Val	Tyr	Val	Leu	Ser	Gly	Lys	Gln	Ile		
	35						40					45					
Tyr	Lys	Asp	Met	Thr	Lys	Phe	Trp	Gly	Lys	Leu	Phe	Gly	Ile	Asn	Phe		
	50					55					60						
Ala	Leu	Gly	Val	Ala	Thr	Gly	Leu	Thr	Met	Glu	Phe	Gln	Phe	Gly	Thr		
65					70					75					80		
Asn	Trp	Ser	Tyr	Tyr	Ser	His	Tyr	Val	Gly	Asp	Ile	Phe	Gly	Ala	Pro		
			85					90						95			
Leu	Ala	Ile	Glu	Gly	Leu	Met	Ala	Phe	Phe	Leu	Glu	Ser	Thr	Phe	Val		
	100							105					110				
Gly	Leu	Phe	Phe	Gly	Trp	Asp	Arg	Leu	Gly	Lys	Val	Gln	His	Met			
	115					120					125						
Cys	Val	Thr	Trp	Leu	Val	Ala	Leu	Gly	Ser	Asn	Leu	Ser	Ala	Leu	Trp		
	130					135					140						
Ile	Leu	Val	Ala	Asn	Gly	Trp	Met	Gln	Asn	Pro	Ile	Ala	Ser	Asp	Phe		
145				150					155						160		
Asn	Phe	Glu	Thr	Met	Arg	Met	Glu	Met	Val	Ser	Phe	Ser	Glu	Leu	Val		
			165					170						175			
Leu	Asn	Pro	Val	Ala	Gln	Val	Lys	Phe	Val	His	Thr	Val	Ala	Ser	Gly		
	180							185					190				
Tyr	Val	Thr	Gly	Ala	Met	Phe	Ile	Leu	Gly	Ile	Ser	Ala	Trp	Tyr	Met		
	195					200						205					
Leu	Lys	Gly	Arg	Asp	Phe	Ala	Phe	Ala	Lys	Arg	Ser	Phe	Ala	Ile	Ala		
	210				215						220						
Ala	Ser	Phe	Gly	Met	Ala	Ala	Val	Leu	Ser	Val	Ile	Val	Leu	Gly	Asp		
225					230				235						240		

Glu Ser Gly Tyr Glu Met Gly Asp Val Gln Lys Thr Lys Leu Ala Ala
 245 250 255
 Ile Glu Ala Glu Trp Glu Thr Gln Pro Ala Pro Ala Ala Phe Thr Leu
 260 265 270
 Phe Gly Ile Pro Asp Gln Glu Glu Thr Asn Lys Phe Ala Ile Gln
 275 280 285
 Ile Pro Tyr Ala Leu Gly Ile Ile Ala Thr Arg Ser Val Asp Thr Pro
 290 295 300
 Val Ile Gly Leu Lys Glu Leu Met Val Gln His Glu Glu Arg Ile Arg
 305 310 315 320
 Asn Gly Met Lys Ala Tyr Ser Leu Leu Glu Gln Leu Arg Ser Gly Ser
 325 330 335
 Thr Asp Gln Ala Val Arg Asp Gln Phe Asn Ser Met Lys Lys Asp Leu
 340 345 350
 Gly Tyr Gly Leu Leu Leu Lys Arg Tyr Thr Pro Asn Val Ala Asp Ala
 355 360 365
 Thr Glu Ala Gln Ile Gln Gln Ala Thr Lys Asp Ser Ile Pro Arg Val
 370 375 380
 Ala Pro Leu Tyr Phe Ala Phe Arg Ile Met Val Ala Cys Gly Phe Leu
 385 390 395 400
 Leu Leu Ala Ile Ile Ala Leu Ser Phe Trp Ser Val Ile Arg Asn Arg
 405 410 415
 Ile Gly Glu Lys Lys Trp Leu Leu Arg Ala Ala Leu Tyr Gly Ile Pro
 420 425 430
 Leu Pro Trp Ile Ala Val Glu Ala Gly Trp Phe Val Ala Glu Tyr Gly
 435 440 445
 Arg Gln Pro Trp Ala Ile Gly Glu Val Leu Pro Thr Ala Val Ala Asn
 450 455 460
 Ser Ser Leu Thr Ala Gly Asp Leu Ile Phe Ser Met Val Leu Ile Cys
 465 470 475 480
 Gly Leu Tyr Thr Leu Phe Leu Val Ala Glu Leu Phe Leu Met Phe Lys
 485 490 495
 Phe Ala Arg Leu Gly Pro Ser Ser Leu Lys Thr Gly Arg Tyr His Phe
 500 505 510
 Glu Gln Ser Ser Thr Thr Thr Gln Pro Ala Arg
 515 520

<210> 355
 <211> 379
 <212> PRT
 <213> E. Coli

<400> 355
 Met Ile Asp Tyr Glu Val Leu Arg Phe Ile Trp Trp Leu Leu Val Gly
 1 5 10 15
 Val Leu Leu Ile Gly Phe Ala Val Thr Asp Gly Phe Asp Met Gly Val
 20 25 30
 Gly Met Leu Thr Arg Phe Leu Gly Arg Asn Asp Thr Glu Arg Arg Ile
 35 40 45
 Met Ile Asn Ser Ile Ala Pro His Trp Asp Gly Asn Gln Val Trp Leu
 50 55 60
 Ile Thr Ala Gly Gly Ala Leu Phe Ala Ala Trp Pro Met Val Tyr Ala
 65 70 75 80
 Ala Ala Phe Ser Gly Phe Tyr Val Ala Met Ile Leu Val Leu Ala Ser
 85 90 95
 Leu Phe Phe Arg Pro Val Gly Phe Asp Tyr Arg Ser Lys Ile Glu Glu

<210> 356
 <211> 456
 <212> PRT
 <213> E. Coli

<400> 356
 Met Glu Leu Ser Ser Leu Thr Ala Val Ser Pro Val Asp Gly Arg Tyr
 1 5 10 15
 Gly Asp Lys Val Ser Ala Leu Arg Gly Ile Phe Ser Glu Tyr Gly Leu
 20 25 30
 Leu Lys Phe Arg Val Gln Val Glu Val Arg Trp Leu Gln Lys Leu Ala
 35 40 45
 Ala His Ala Ala Ile Lys Glu Val Pro Ala Phe Ala Ala Asp Ala Ile
 50 55 60
 Gly Tyr Leu Asp Ala Ile Val Ala Ser Phe Ser Glu Glu Asp Ala Ala
 65 70 75 80
 Arg Ile Lys Thr Ile Glu Arg Thr Thr Asn His Asp Val Lys Ala Val
 85 90 95
 Glu Tyr Phe Leu Lys Glu Lys Val Ala Glu Ile Pro Glu Leu His Ala
 100 105 110

Val	Ser	Glu	Phe	Ile	His	Phe	Ala	Cys	Thr	Ser	Glu	Asp	Ile	Asn	Asn		
	115						120					125					
Leu	Ser	His	Ala	Leu	Met	Leu	Lys	Thr	Ala	Arg	Asp	Glu	Val	Ile	Leu		
	130						135					140					
Pro	Tyr	Trp	Arg	Gln	Leu	Ile	Asp	Gly	Ile	Lys	Asp	Leu	Ala	Val	Gln		
145					150					155					160		
Tyr	Arg	Asp	Ile	Pro	Leu	Leu	Ser	Arg	Thr	His	Gly	Gln	Pro	Ala	Thr		
				165					170						175		
Pro	Ser	Thr	Ile	Gly	Lys	Glu	Met	Ala	Asn	Val	Ala	Tyr	Arg	Met	Glu		
			180					185						190			
Arg	Gln	Tyr	Arg	Gln	Leu	Asn	Gln	Val	Glu	Ile	Leu	Gly	Lys	Ile	Asn		
		195					200						205				
Gly	Ala	Val	Gly	Asn	Tyr	Asn	Ala	His	Ile	Ala	Ala	Tyr	Pro	Glu	Val		
	210					215						220					
Asp	Trp	His	Gln	Phe	Ser	Glu	Glu	Phe	Val	Thr	Ser	Leu	Gly	Ile	Gln		
225					230					235					240		
Trp	Asn	Pro	Tyr	Thr	Thr	Gln	Ile	Glu	Pro	His	Asp	Tyr	Ile	Ala	Glu		
				245					250						255		
Leu	Phe	Asp	Cys	Val	Ala	Arg	Phe	Asn	Thr	Ile	Leu	Ile	Asp	Phe	Asp		
			260					265						270			
Arg	Asp	Val	Trp	Gly	Tyr	Ile	Ala	Leu	Asn	His	Phe	Lys	Gln	Lys	Thr		
		275					280						285				
Ile	Ala	Gly	Glu	Ile	Gly	Ser	Ser	Thr	Met	Pro	His	Lys	Val	Asn	Pro		
	290					295						300					
Ile	Asp	Phe	Glu	Asn	Ser	Glu	Gly	Asn	Leu	Gly	Leu	Ser	Asn	Ala	Val		
305					310					315					320		
Leu	Gln	His	Leu	Ala	Ser	Lys	Leu	Pro	Val	Ser	Arg	Trp	Gln	Arg	Asp		
				325					330						335		
Leu	Thr	Asp	Ser	Thr	Val	Leu	Arg	Asn	Leu	Gly	Val	Gly	Ile	Gly	Tyr		
			340					345						350			
Ala	Leu	Ile	Ala	Tyr	Gln	Ser	Thr	Leu	Lys	Gly	Val	Ser	Lys	Leu	Glu		
		355					360							365			
Val	Asn	Arg	Asp	His	Leu	Leu	Asp	Glu	Leu	Asp	His	Asn	Trp	Glu	Val		
	370					375						380					
Leu	Ala	Glu	Pro	Ile	Gln	Thr	Val	Met	Arg	Arg	Tyr	Gly	Ile	Glu	Lys		
385					390					395					400		
Pro	Tyr	Glu	Lys	Leu	Lys	Glu	Leu	Thr	Arg	Gly	Lys	Arg	Val	Asp	Ala		
				405					410						415		
Glu	Gly	Met	Lys	Gln	Phe	Ile	Asp	Gly	Leu	Ala	Leu	Pro	Glu	Glu	Glu		
			420					425						430			
Lys	Ala	Arg	Leu	Lys	Ala	Met	Thr	Pro	Ala	Asn	Tyr	Ile	Gly	Arg	Ala		
		435					440						445				
Ile	Thr	Met	Val	Asp	Glu	Leu	Lys										
	450					455											

<210> 357
 <211> 61
 <212> PRT
 <213> E. Coli

<400> 357

Met	Leu	Ile	Leu	Thr	Arg	Arg	Val	Gly	Glu	Thr	Leu	Met	Ile	Gly	Asp		
1				5					10					15			
Glu	Val	Thr	Val	Thr	Val	Leu	Gly	Val	Lys	Gly	Asn	Gln	Val	Arg	Ile		
			20					25					30				
Gly	Val	Asn	Ala	Pro	Lys	Glu	Val	Ser	Val	His	Arg	Glu	Glu	Ile	Tyr		

	35		40		45
Gln	Arg	Ile	Gln	Ala	Glu
			Lys	Ser	Gln
				Gln	Ser
				Ser	Tyr
	50		55		60

<210> 358
 <211> 93
 <212> RNA
 <213> E. Coli

<400> 358	
ggugaggugg ccgagaggcu gaaggcgcuc ccugcuaag ggaguaugcg gucaaaagcu	60
gcauccgggg uucgaauccc cgccucaccg cca	93

<210> 359
 <211> 200
 <212> PRT
 <213> E. Coli

<400> 359	
Met Lys Asn Lys Ala Asp Asn Lys Lys Arg Asn Phe Leu Thr His Ser	
1 5 10 15	
Glu Ile Glu Ser Leu Leu Lys Ala Ala Asn Thr Gly Pro His Ala Ala	
20 25 30	
Arg Asn Tyr Cys Leu Thr Leu Leu Cys Phe Ile His Gly Phe Arg Ala	
35 40 45	
Ser Glu Ile Cys Arg Leu Arg Ile Ser Asp Ile Asp Leu Lys Ala Lys	
50 55 60	
Cys Ile Tyr Ile His Arg Leu Lys Lys Gly Phe Ser Thr Thr His Pro	
65 70 75 80	
Leu Leu Asn Lys Glu Val Gln Ala Leu Lys Asn Trp Leu Ser Ile Arg	
85 90 95	
Thr Ser Tyr Pro His Ala Glu Ser Glu Trp Val Phe Leu Ser Arg Lys	
100 105 110	
Gly Asn Pro Leu Ser Arg Gln Gln Phe Tyr His Ile Ile Ser Thr Ser	
115 120 125	
Gly Gly Asn Ala Gly Leu Ser Leu Glu Ile His Pro His Met Leu Arg	
130 135 140	
His Ser Cys Gly Phe Ala Leu Ala Asn Met Gly Ile Asp Thr Arg Leu	
145 150 155 160	
Ile Gln Asp Tyr Leu Gly His Arg Asn Ile Arg His Thr Val Trp Tyr	
165 170 175	
Thr Ala Ser Asn Ala Gly Arg Phe Tyr Gly Ile Trp Asp Arg Ala Arg	
180 185 190	
Gly Arg Gln Arg His Ala Val Leu	
195 200	

<210> 360
 <211> 198
 <212> PRT
 <213> E. Coli

<400> 360	
Met Ser Lys Arg Arg Tyr Leu Thr Gly Lys Glu Val Gln Ala Met Met	
1 5 10 15	

Gln	Ala	Val	Cys	Tyr	Gly	Ala	Thr	Gly	Ala	Arg	Asp	Tyr	Cys	Leu	Ile
		20						25					30		
Leu	Leu	Ala	Tyr	Arg	His	Gly	Met	Arg	Ile	Ser	Glu	Leu	Leu	Asp	Leu
		35					40					45			
His	Tyr	Gln	Asp	Leu	Asp	Leu	Asn	Glu	Gly	Arg	Ile	Asn	Ile	Arg	Arg
	50					55					60				
Leu	Lys	Asn	Gly	Phe	Ser	Thr	Val	His	Pro	Leu	Arg	Phe	Asp	Glu	Arg
65					70					75					80
Glu	Ala	Val	Glu	Arg	Trp	Thr	Gln	Glu	Arg	Ala	Asn	Trp	Lys	Gly	Ala
			85						90					95	
Asp	Arg	Thr	Asp	Ala	Ile	Phe	Ile	Ser	Arg	Arg	Gly	Ser	Arg	Leu	Ser
			100					105					110		
Arg	Gln	Gln	Ala	Tyr	Arg	Ile	Ile	Arg	Asp	Ala	Gly	Ile	Glu	Ala	Gly
		115					120					125			
Thr	Val	Thr	Gln	Thr	His	Pro	His	Met	Leu	Arg	His	Ala	Cys	Gly	Tyr
	130					135					140				
Glu	Leu	Ala	Glu	Arg	Gly	Ala	Asp	Thr	Arg	Leu	Ile	Gln	Asp	Tyr	Leu
145					150					155					160
Gly	His	Arg	Asn	Ile	Arg	His	Thr	Val	Arg	Tyr	Thr	Ala	Ser	Asn	Ala
			165						170					175	
Ala	Arg	Phe	Ala	Gly	Leu	Trp	Glu	Arg	Asn	Asn	Leu	Ile	Asn	Glu	Lys
		180						185					190		
Leu	Lys	Arg	Glu	Glu	Val										
		195													

<210> 361
 <211> 182
 <212> PRT
 <213> E. Coli

<400> 361

Met	Lys	Ile	Lys	Thr	Leu	Ala	Ile	Val	Val	Leu	Ser	Ala	Leu	Ser	Leu
1			5						10				15		
Ser	Ser	Thr	Ala	Ala	Leu	Ala	Ala	Ala	Thr	Thr	Val	Asn	Gly	Gly	Thr
		20						25				30			
Val	His	Phe	Lys	Gly	Glu	Val	Val	Asn	Ala	Ala	Cys	Ala	Val	Asp	Ala
	35					40					45				
Gly	Ser	Val	Asp	Gln	Thr	Val	Gln	Leu	Gly	Gln	Val	Arg	Thr	Ala	Ser
	50					55				60					
Leu	Ala	Gln	Glu	Gly	Ala	Thr	Ser	Ser	Ala	Val	Gly	Phe	Asn	Ile	Gln
65					70					75					80
Leu	Asn	Asp	Cys	Asp	Thr	Asn	Val	Ala	Ser	Lys	Ala	Ala	Val	Ala	Phe
			85						90					95	
Leu	Gly	Thr	Ala	Ile	Asp	Ala	Gly	His	Thr	Asn	Val	Leu	Ala	Leu	Gln
			100					105					110		
Ser	Ser	Ala	Ala	Gly	Ser	Ala	Thr	Asn	Val	Gly	Val	Gln	Ile	Leu	Asp
		115					120					125			
Arg	Thr	Gly	Ala	Ala	Leu	Thr	Leu	Asp	Gly	Ala	Thr	Phe	Ser	Ser	Glu
	130					135					140				
Thr	Thr	Leu	Asn	Asn	Gly	Thr	Asn	Thr	Ile	Pro	Phe	Gln	Ala	Arg	Tyr
145					150					155					160
Phe	Ala	Thr	Gly	Ala	Ala	Thr	Pro	Gly	Ala	Ala	Asn	Ala	Asp	Ala	Thr
			165						170					175	
Phe	Lys	Val	Gln	Tyr	Gln										
			180												

<210> 362
 <211> 215
 <212> PRT
 <213> E. Coli

<400> 362

Met	Leu	Leu	Met	Arg	Met	Arg	Pro	Ser	Arg	Phe	Ser	Ile	Asn	Asn	Leu
1			5					10					15		
Pro	Arg	Phe	Arg	Asp	Val	Ile	Thr	Gly	Arg	Asp	Ala	His	Pro	Cys	Ala
			20					25					30		
Ile	Lys	Ile	Thr	Met	Lys	Arg	Lys	Arg	Leu	Phe	Leu	Leu	Ala	Ser	Leu
		35					40					45			
Leu	Pro	Met	Phe	Ala	Leu	Ala	Gly	Asn	Lys	Trp	Asn	Thr	Thr	Leu	Pro
	50					55					60				
Gly	Gly	Asn	Met	Gln	Phe	Gln	Gly	Val	Ile	Ile	Ala	Glu	Thr	Cys	Arg
65				70						75					80
Ile	Glu	Ala	Gly	Asp	Lys	Gln	Met	Thr	Val	Asn	Met	Gly	Gln	Ile	Ser
				85					90					95	
Ser	Asn	Arg	Phe	His	Ala	Val	Gly	Glu	Asp	Ser	Ala	Pro	Val	Pro	Phe
			100					105					110		
Val	Ile	His	Leu	Arg	Glu	Cys	Ser	Thr	Val	Val	Ser	Glu	Arg	Val	Gly
		115					120					125			
Val	Ala	Phe	His	Gly	Val	Ala	Asp	Gly	Lys	Asn	Pro	Asp	Val	Leu	Ser
	130					135					140				
Val	Gly	Glu	Gly	Pro	Gly	Ile	Ala	Thr	Asn	Ile	Gly	Val	Ala	Leu	Phe
145					150					155					160
Asp	Asp	Glu	Gly	Asn	Leu	Val	Pro	Ile	Asn	Arg	Pro	Pro	Ala	Asn	Trp
				165					170					175	
Lys	Arg	Leu	Tyr	Ser	Gly	Ser	Thr	Ser	Leu	His	Phe	Ile	Ala	Lys	Tyr
			180					185					190		
Arg	Ala	Thr	Gly	Arg	Arg	Val	Thr	Gly	Gly	Ile	Ala	Asn	Ala	Gln	Ala
		195					200					205			
Trp	Phe	Ser	Leu	Thr	Tyr	Gln									
	210					215									

<210> 363
 <211> 241
 <212> PRT
 <213> E. Coli

<400> 363

Met	Ser	Asn	Lys	Asn	Val	Asn	Val	Arg	Lys	Ser	Gln	Glu	Ile	Thr	Phe
1			5					10					15		
Cys	Leu	Leu	Ala	Gly	Ile	Leu	Met	Phe	Met	Ala	Met	Met	Val	Ala	Gly
			20					25					30		
Arg	Ala	Glu	Ala	Gly	Val	Ala	Leu	Gly	Ala	Thr	Arg	Val	Ile	Tyr	Pro
		35					40					45			
Ala	Gly	Gln	Lys	Gln	Glu	Gln	Leu	Ala	Val	Thr	Asn	Asn	Asp	Glu	Asn
	50					55					60				
Ser	Thr	Tyr	Leu	Ile	Gln	Ser	Trp	Val	Glu	Asn	Ala	Asp	Gly	Val	Lys
65				70						75					80
Asp	Gly	Arg	Phe	Ile	Val	Thr	Pro	Pro	Leu	Phe	Ala	Met	Lys	Gly	Lys
				85					90					95	

Lys	Glu	Asn	Thr	Leu	Arg	Ile	Leu	Asp	Ala	Thr	Asn	Asn	Gln	Leu	Pro
			100					105					110		
Gln	Asp	Arg	Glu	Ser	Leu	Phe	Trp	Met	Asn	Val	Lys	Ala	Ile	Pro	Ser
	115						120					125			
Met	Asp	Lys	Ser	Lys	Leu	Thr	Glu	Asn	Thr	Leu	Gln	Leu	Ala	Ile	Ile
	130					135					140				
Ser	Arg	Ile	Lys	Leu	Tyr	Tyr	Arg	Pro	Ala	Lys	Leu	Ala	Leu	Pro	Pro
145				150						155					160
Asp	Gln	Ala	Ala	Glu	Lys	Leu	Arg	Phe	Arg	Arg	Ser	Ala	Asn	Ser	Leu
			165					170						175	
Thr	Leu	Ile	Asn	Pro	Thr	Pro	Tyr	Tyr	Leu	Thr	Val	Thr	Glu	Leu	Asn
			180					185					190		
Ala	Gly	Thr	Arg	Val	Leu	Glu	Asn	Ala	Leu	Val	Pro	Pro	Met	Gly	Glu
	195						200					205			
Ser	Thr	Val	Lys	Leu	Pro	Ser	Asp	Ala	Gly	Ser	Asn	Ile	Thr	Tyr	Arg
	210					215					220				
Thr	Ile	Asn	Asp	Tyr	Gly	Ala	Leu	Thr	Pro	Lys	Met	Thr	Gly	Val	Met
225				230						235					240
Glu															

<210> 364
 <211> 878
 <212> PRT
 <213> E. Coli

<400> 364

Met	Ser	Tyr	Leu	Asn	Leu	Arg	Leu	Tyr	Gln	Arg	Asn	Thr	Gln	Cys	Leu
1				5					10					15	
His	Ile	Arg	Lys	His	Arg	Leu	Ala	Gly	Phe	Phe	Val	Arg	Leu	Val	Val
			20					25					30		
Ala	Cys	Ala	Phe	Ala	Ala	Gln	Ala	Pro	Leu	Ser	Ser	Ala	Asp	Leu	Tyr
	35					40						45			
Phe	Asn	Pro	Arg	Phe	Leu	Ala	Asp	Asp	Pro	Gln	Ala	Val	Ala	Asp	Leu
	50					55					60				
Ser	Arg	Phe	Glu	Asn	Gly	Gln	Glu	Leu	Pro	Pro	Gly	Thr	Tyr	Arg	Val
65				70						75					80
Asp	Ile	Tyr	Leu	Asn	Asn	Gly	Tyr	Met	Ala	Thr	Arg	Asp	Val	Thr	Phe
				85					90					95	
Asn	Thr	Gly	Asp	Ser	Glu	Gln	Gly	Ile	Val	Pro	Cys	Leu	Thr	Arg	Ala
		100						105					110		
Gln	Leu	Ala	Ser	Met	Gly	Leu	Asn	Thr	Ala	Ser	Val	Ala	Gly	Met	Asn
	115					120						125			
Leu	Leu	Ala	Asp	Asp	Ala	Cys	Val	Pro	Leu	Thr	Thr	Met	Val	Gln	Asp
	130					135					140				
Ala	Thr	Ala	His	Leu	Asp	Val	Gly	Gln	Gln	Arg	Leu	Asn	Leu	Thr	Ile
145				150						155					160
Pro	Gln	Ala	Phe	Met	Ser	Asn	Arg	Ala	Arg	Gly	Tyr	Ile	Pro	Pro	Glu
			165						170					175	
Leu	Trp	Asp	Pro	Gly	Ile	Asn	Ala	Gly	Leu	Leu	Asn	Tyr	Asn	Phe	Ser
		180						185					190		
Gly	Asn	Ser	Val	Gln	Asn	Arg	Ile	Gly	Gly	Asn	Ser	His	Tyr	Ala	Tyr
	195					200						205			
Leu	Asn	Leu	Gln	Ser	Gly	Leu	Asn	Ile	Gly	Ala	Trp	Arg	Leu	Arg	Asp
	210					215					220				
Asn	Thr	Thr	Trp	Ser	Tyr	Asn	Ser	Ser	Asp	Arg	Ser	Ser	Gly	Ser	Lys

225	Asn	Lys	Trp	Gln	His	Ile	Asn	Thr	Trp	Leu	Glu	Arg	Asp	Ile	Ile	Pro
					245					250						255
Leu	Arg	Ser	Arg	Leu	Thr	Leu	Gly	Asp	Gly	Tyr	Thr	Gln	Gly	Asp	Ile	
			260					265								270
Phe	Asp	Gly	Ile	Asn	Phe	Arg	Gly	Ala	Gln	Leu	Ala	Ser	Asp	Asp	Asn	
		275					280						285			
Met	Leu	Pro	Asp	Ser	Gln	Arg	Gly	Phe	Ala	Pro	Val	Ile	His	Gly	Ile	
	290					295					300					
Ala	Arg	Gly	Thr	Ala	Gln	Val	Thr	Ile	Lys	Gln	Asn	Gly	Tyr	Asp	Ile	
305					310					315						320
Tyr	Asn	Ser	Thr	Val	Pro	Pro	Gly	Pro	Phe	Thr	Ile	Asn	Asp	Ile	Tyr	
				325					330							335
Ala	Ala	Gly	Asn	Ser	Gly	Asp	Leu	Gln	Val	Thr	Ile	Lys	Glu	Ala	Asp	
			340					345					350			
Gly	Ser	Thr	Gln	Ile	Phe	Thr	Val	Pro	Tyr	Ser	Ser	Val	Pro	Leu	Leu	
		355					360						365			
Gln	Arg	Glu	Gly	His	Thr	Arg	Tyr	Ser	Ile	Thr	Ala	Gly	Glu	Tyr	Arg	
370						375						380				
Ser	Gly	Asn	Ala	Gln	Gln	Glu	Lys	Thr	Arg	Phe	Phe	Gln	Ser	Thr	Leu	
385					390					395						400
Leu	His	Gly	Leu	Pro	Ala	Gly	Trp	Thr	Ile	Tyr	Gly	Gly	Thr	Gln	Leu	
				405					410							415
Ala	Asp	Arg	Tyr	Arg	Ala	Phe	Asn	Phe	Gly	Ile	Gly	Lys	Asn	Met	Gly	
			420					425					430			
Ala	Leu	Gly	Ala	Leu	Ser	Val	Asp	Met	Thr	Gln	Ala	Asn	Ser	Thr	Leu	
		435					440						445			
Pro	Asp	Asp	Ser	Gln	His	Asp	Gly	Gln	Ser	Val	Arg	Phe	Leu	Tyr	Asn	
	450					455						460				
Lys	Ser	Leu	Asn	Glu	Ser	Gly	Thr	Asn	Ile	Gln	Leu	Val	Gly	Tyr	Arg	
465					470					475						480
Tyr	Ser	Thr	Ser	Gly	Tyr	Phe	Asn	Phe	Ala	Asp	Thr	Thr	Tyr	Ser	Arg	
				485					490							495
Met	Asn	Gly	Tyr	Asn	Ile	Glu	Thr	Gln	Asp	Gly	Val	Ile	Gln	Val	Lys	
		500						505					510			
Pro	Lys	Phe	Thr	Asp	Tyr	Tyr	Asn	Leu	Ala	Tyr	Asn	Lys	Arg	Gly	Lys	
		515					520					525				
Leu	Gln	Leu	Thr	Val	Thr	Gln	Gln	Leu	Gly	Arg	Thr	Ser	Thr	Leu	Tyr	
	530					535					540					
Leu	Ser	Gly	Ser	His	Gln	Thr	Tyr	Trp	Gly	Thr	Ser	Asn	Val	Asp	Glu	
545					550					555						560
Gln	Phe	Gln	Ala	Gly	Leu	Asn	Thr	Ala	Phe	Glu	Asp	Ile	Asn	Trp	Thr	
			565						570							575
Leu	Ser	Tyr	Ser	Leu	Thr	Lys	Asn	Ala	Trp	Gln	Lys	Gly	Arg	Asp	Gln	
		580						585					590			
Met	Leu	Ala	Leu	Asn	Val	Asn	Ile	Pro	Phe	Ser	His	Trp	Leu	Arg	Ser	
		595					600					605				
Asp	Ser	Lys	Ser	Gln	Trp	Arg	His	Ala	Ser	Ala	Ser	Tyr	Ser	Met	Ser	
	610					615					620					
His	Asp	Leu	Asn	Gly	Arg	Met	Thr	Asn	Leu	Ala	Gly	Val	Tyr	Gly	Thr	
625					630					635						640
Leu	Leu	Glu	Asp	Asn	Asn	Leu	Ser	Tyr	Ser	Val	Gln	Thr	Gly	Tyr	Ala	
				645					650							655
Gly	Gly	Gly	Asp	Gly	Asn	Ser	Gly	Ser	Thr	Gly	Tyr	Ala	Thr	Leu	Asn	
			660					665								670
Tyr	Arg	Gly	Gly	Tyr	Gly	Asn	Ala	Asn	Ile	Gly	Tyr	Ser	His	Ser	Asp	
		675					680									685

Asp	Ile	Lys	Gln	Leu	Tyr	Tyr	Gly	Val	Ser	Gly	Gly	Val	Leu	Ala	His	
690						695					700					
Ala	Asn	Gly	Val	Thr	Leu	Gly	Gln	Pro	Leu	Asn	Asp	Thr	Val	Val	Leu	
705					710					715					720	
Val	Lys	Ala	Pro	Gly	Ala	Lys	Asp	Ala	Lys	Val	Glu	Asn	Gln	Thr	Gly	
				725					730					735		
Val	Arg	Thr	Asp	Trp	Arg	Gly	Tyr	Ala	Val	Leu	Pro	Tyr	Ala	Thr	Glu	
			740					745					750			
Tyr	Arg	Glu	Asn	Arg	Val	Ala	Leu	Asp	Thr	Asn	Thr	Leu	Ala	Asp	Asn	
		755					760					765				
Val	Asp	Leu	Asp	Asn	Ala	Val	Ala	Asn	Val	Val	Pro	Thr	Arg	Gly	Ala	
	770					775					780					
Ile	Val	Arg	Ala	Glu	Phe	Lys	Ala	Arg	Val	Gly	Ile	Lys	Leu	Leu	Met	
785					790					795					800	
Thr	Leu	Thr	His	Asn	Asn	Lys	Pro	Leu	Pro	Phe	Gly	Ala	Met	Val	Thr	
				805					810					815		
Ser	Glu	Ser	Ser	Gln	Ser	Ser	Gly	Ile	Val	Ala	Asp	Asn	Gly	Gln	Val	
			820				825						830			
Tyr	Leu	Ser	Gly	Met	Pro	Leu	Ala	Gly	Lys	Val	Gln	Val	Lys	Trp	Gly	
	835						840						845			
Glu	Glu	Glu	Asn	Ala	His	Cys	Val	Ala	Asn	Tyr	Gln	Leu	Pro	Pro	Glu	
	850					855					860					
Ser	Gln	Gln	Gln	Leu	Leu	Thr	Gln	Leu	Ser	Ala	Glu	Cys	Arg			
865					870					875						

<210> 365
 <211> 176
 <212> PRT
 <213> E. Coli

<400> 365

Met	Arg	Asn	Lys	Pro	Phe	Tyr	Leu	Leu	Cys	Ala	Phe	Leu	Trp	Leu	Ala	
1				5					10					15		
Val	Ser	His	Ala	Leu	Ala	Ala	Asp	Ser	Thr	Ile	Thr	Ile	Arg	Gly	Tyr	
			20					25					30			
Val	Arg	Asp	Asn	Gly	Cys	Ser	Val	Ala	Ala	Glu	Ser	Thr	Asn	Phe	Thr	
		35					40					45				
Val	Asp	Leu	Met	Glu	Asn	Ala	Ala	Lys	Gln	Phe	Asn	Asn	Ile	Gly	Ala	
	50					55					60					
Thr	Thr	Pro	Val	Val	Pro	Phe	Arg	Ile	Leu	Leu	Ser	Pro	Cys	Gly	Asn	
65					70					75					80	
Ala	Val	Ser	Ala	Val	Lys	Val	Gly	Phe	Thr	Gly	Val	Ala	Asp	Ser	His	
			85						90					95		
Asn	Ala	Asn	Leu	Leu	Ala	Leu	Glu	Asn	Thr	Val	Ser	Ala	Ala	Ser	Gly	
			100					105					110			
Leu	Gly	Ile	Gln	Leu	Leu	Asn	Glu	Gln	Gln	Asn	Gln	Ile	Pro	Leu	Asn	
	115						120					125				
Ala	Pro	Ser	Ser	Ala	Leu	Ser	Trp	Thr	Thr	Leu	Thr	Pro	Gly	Lys	Pro	
	130					135					140					
Asn	Thr	Leu	Asn	Phe	Tyr	Ala	Arg	Leu	Met	Ala	Thr	Gln	Val	Pro	Val	
145				150					155						160	
Thr	Ala	Gly	His	Ile	Asn	Ala	Thr	Ala	Thr	Phe	Thr	Leu	Glu	Tyr	Gln	
				165					170						175	

<210> 366
 <211> 167
 <212> PRT
 <213> E. Coli

<400> 366

Met	Lys	Trp	Cys	Lys	Arg	Gly	Tyr	Val	Leu	Ala	Ala	Ile	Leu	Ala	Leu
1				5					10					15	
Ala	Ser	Ala	Thr	Ile	Gln	Ala	Ala	Asp	Val	Thr	Ile	Thr	Val	Asn	Gly
			20					25					30		
Lys	Val	Val	Ala	Lys	Pro	Cys	Thr	Val	Ser	Thr	Thr	Asn	Ala	Thr	Val
			35				40					45			
Asp	Leu	Gly	Asp	Leu	Tyr	Ser	Phe	Ser	Leu	Met	Ser	Ala	Gly	Ala	Ala
			50			55					60				
Ser	Ala	Trp	His	Asp	Val	Ala	Leu	Glu	Leu	Thr	Asn	Cys	Pro	Val	Gly
65				70						75					80
Thr	Ser	Arg	Val	Thr	Ala	Ser	Phe	Ser	Gly	Ala	Ala	Asp	Ser	Thr	Gly
				85					90					95	
Tyr	Tyr	Lys	Asn	Gln	Gly	Thr	Ala	Gln	Asn	Ile	Gln	Leu	Glu	Leu	Gln
			100					105					110		
Asp	Asp	Ser	Gly	Asn	Thr	Leu	Asn	Thr	Gly	Ala	Thr	Lys	Thr	Val	Gln
			115				120					125			
Val	Asp	Asp	Ser	Ser	Gln	Ser	Ala	His	Phe	Pro	Leu	Gln	Val	Arg	Ala
			130			135					140				
Leu	Thr	Val	Asn	Gly	Gly	Ala	Thr	Gln	Gly	Thr	Ile	Gln	Ala	Val	Ile
145				150						155					160
Ser	Ile	Thr	Tyr	Thr	Tyr	Ser									
				165											

<210> 367
 <211> 300
 <212> PRT
 <213> E. Coli

<400> 367

Met	Lys	Arg	Val	Ile	Thr	Leu	Phe	Ala	Val	Leu	Leu	Met	Gly	Trp	Ser
1				5					10					15	
Val	Asn	Ala	Trp	Ser	Phe	Ala	Cys	Lys	Thr	Ala	Asn	Gly	Thr	Ala	Ile
			20					25					30		
Pro	Ile	Gly	Gly	Gly	Ser	Ala	Asn	Val	Tyr	Val	Asn	Leu	Ala	Pro	Val
			35				40					45			
Val	Asn	Val	Gly	Gln	Asn	Leu	Val	Val	Asp	Leu	Ser	Thr	Gln	Ile	Phe
			50			55					60				
Cys	His	Asn	Asp	Tyr	Pro	Glu	Thr	Ile	Thr	Asp	Tyr	Val	Thr	Leu	Gln
65				70						75					80
Arg	Gly	Ser	Ala	Tyr	Gly	Gly	Val	Leu	Ser	Asn	Phe	Ser	Gly	Thr	Val
				85					90					95	
Lys	Tyr	Ser	Gly	Ser	Ser	Tyr	Pro	Phe	Pro	Thr	Thr	Ser	Glu	Thr	Pro
			100					105					110		
Arg	Val	Val	Tyr	Asn	Ser	Arg	Thr	Asp	Lys	Pro	Trp	Pro	Val	Ala	Leu
			115				120					125			
Tyr	Leu	Thr	Pro	Val	Ser	Ser	Ala	Gly	Gly	Val	Ala	Ile	Lys	Ala	Gly
			130			135					140				
Ser	Leu	Ile	Ala	Val	Leu	Ile	Leu	Arg	Gln	Thr	Asn	Asn	Tyr	Asn	Ser
145				150						155					160

Asp	Asp	Phe	Gln	Phe	Val	Trp	Asn	Ile	Tyr	Ala	Asn	Asn	Asp	Val	Val
			165						170					175	
Val	Pro	Thr	Gly	Gly	Cys	Asp	Val	Ser	Ala	Arg	Asp	Val	Thr	Val	Thr
			180						185					190	
Leu	Pro	Asp	Tyr	Pro	Gly	Ser	Val	Pro	Ile	Pro	Leu	Thr	Val	Tyr	Cys
			195					200					205		
Ala	Lys	Ser	Gln	Asn	Leu	Gly	Tyr	Tyr	Leu	Ser	Gly	Thr	Thr	Ala	Asp
			210			215					220				
Ala	Gly	Asn	Ser	Ile	Phe	Thr	Asn	Thr	Ala	Ser	Phe	Ser	Pro	Ala	Gln
			225		230					235					240
Gly	Val	Gly	Val	Gln	Leu	Thr	Arg	Asn	Gly	Thr	Ile	Ile	Pro	Ala	Asn
				245					250						255
Asn	Thr	Val	Ser	Leu	Gly	Ala	Val	Gly	Thr	Ser	Ala	Val	Ser	Leu	Gly
			260					265					270		
Leu	Thr	Ala	Asn	Tyr	Ala	Arg	Thr	Gly	Gly	Gln	Val	Thr	Ala	Gly	Asn
			275				280					285			
Val	Gln	Ser	Ile	Ile	Gly	Val	Thr	Phe	Val	Tyr	Gln				
			290			295					300				

<210> 368
 <211> 521
 <212> PRT
 <213> E. Coli

<400> 368

Met	Leu	Ser	Lys	Leu	Pro	Arg	Arg	Leu	Arg	Ser	Phe	Gln	Thr	Tyr	Cys
1				5					10					15	
Thr	Ile	Arg	Val	His	Arg	Gly	Glu	Asp	Met	Lys	Ser	Met	Asp	Lys	Leu
			20					25					30		
Thr	Thr	Gly	Val	Ala	Tyr	Gly	Thr	Ser	Ala	Gly	Asn	Ala	Gly	Phe	Trp
			35				40					45			
Ala	Leu	Gln	Leu	Leu	Asp	Lys	Val	Thr	Pro	Ser	Gln	Trp	Ala	Ala	Ile
			50			55					60				
Gly	Val	Leu	Gly	Ser	Leu	Val	Phe	Gly	Leu	Leu	Thr	Tyr	Leu	Thr	Asn
			65		70					75					80
Leu	Tyr	Phe	Lys	Ile	Lys	Glu	Asp	Arg	Arg	Lys	Ala	Ala	Arg	Gly	Glu
			85					90					95		
Ser	Asn	Asp	Ser	Arg	Leu	Thr	Gly	Cys	Glu	Arg	Ser	Pro	Phe	Glu	Ser
			100					105					110		
Tyr	Gly	Asn	Cys	Ser	Leu	Thr	Gly	Gln	Arg	Thr	Leu	Arg	Asn	Phe	Pro
			115				120					125			
Gly	Cys	Arg	His	Gly	Pro	Cys	Arg	Ser	Cys	Ala	Gly	Val	Leu	Gly	Ser
			130			135					140				
Ser	Gln	Lys	Glu	Arg	Pro	Ala	Ser	Leu	Pro	Gly	Ser	Ser	Arg	Lys	Ile
			145		150					155					160
Val	Arg	Lys	Ser	Val	Leu	Ser	Ala	Ala	Ser	Val	Leu	Leu	Asp	Lys	Ser
			165						170					175	
Cys	Gln	Ala	Arg	Ala	Ser	Ser	Ser	Ile	Ser	Met	Asn	Thr	Lys	Ile	Arg
			180					185					190		
Tyr	Gly	Leu	Ser	Ala	Ala	Val	Leu	Ala	Leu	Ile	Gly	Ala	Gly	Ala	Ser
			195				200					205			
Ala	Pro	Gln	Ile	Leu	Asp	Gln	Phe	Leu	Asp	Glu	Lys	Glu	Gly	Asn	His
			210			215					220				
Thr	Met	Ala	Tyr	Arg	Asp	Gly	Ser	Gly	Ile	Trp	Thr	Ile	Cys	Arg	Gly
			225		230					235					240

Ala	Thr	Val	Val	Asp	Gly	Lys	Thr	Val	Phe	Pro	Asn	Met	Lys	Leu	Ser
				245					250					255	
Lys	Glu	Lys	Cys	Asp	Gln	Val	Asn	Ala	Ile	Glu	Arg	Asp	Lys	Ala	Leu
			260					265					270		
Ala	Trp	Val	Glu	Arg	Asn	Ile	Lys	Val	Pro	Leu	Thr	Glu	Pro	Gln	Lys
		275					280					285			
Ala	Gly	Ile	Ala	Ser	Phe	Cys	Pro	Tyr	Asn	Ile	Gly	Pro	Gly	Lys	Cys
	290					295					300				
Phe	Pro	Ser	Thr	Phe	Tyr	Lys	Arg	Leu	Asn	Ala	Gly	Asp	Arg	Lys	Gly
305					310					315					320
Ala	Cys	Glu	Ala	Ile	Arg	Trp	Trp	Ile	Lys	Asp	Gly	Gly	Arg	Asp	Cys
				325					330					335	
Arg	Ile	Arg	Ser	Asn	Asn	Cys	Tyr	Gly	Gln	Val	Ile	Arg	Arg	Asp	Gln
			340					345					350		
Glu	Ser	Ala	Leu	Thr	Cys	Trp	Gly	Ile	Glu	Gln	Ile	Arg	Tyr	Ser	Trp
		355					360					365			
Phe	Phe	Ser	Cys	Cys	Gln	Asp	Leu	Ser	Ser	Glu	Met	Ser	Gly	Ala	Thr
	370					375					380				
Glu	Asp	Gly	Lys	Lys	Asn	Gly	Arg	Asn	Val	Met	Leu	Pro	His	Tyr	His
385					390					395					400
Lys	Arg	Met	Leu	Asn	Leu	Leu	Leu	Glu	Leu	Asn	Arg	Gly	Glu	Leu	Pro
				405					410					415	
Val	Met	Arg	Leu	Leu	Lys	Met	Arg	Asn	Arg	Asn	Leu	Leu	Lys	Phe	Leu
			420					425					430		
Pro	Gly	Leu	Leu	Ile	Cys	Leu	Ile	Val	Leu	Thr	Ser	Cys	Val	Pro	Lys
		435					440					445			
Gln	Lys	Asn	Met	Pro	Tyr	Ala	Leu	Thr	Gln	Arg	Ser	Ile	Pro	Gln	Ile
	450					455					460				
Leu	Pro	Leu	Pro	Ser	Glu	Ala	Lys	Gln	Pro	Lys	Pro	Pro	Lys	Glu	Cys
465					470					475					480
Ser	Pro	Thr	Cys	Ser	Glu	Ile	Leu	Gln	Gln	Lys	Leu	Ser	Phe	Met	Leu
			485						490					495	
Lys	Leu	Leu	Thr	Asn	Ala	Thr	Ser	Gln	Glu	Leu	Val	Asn	Arg	Ser	Met
			500					505					510		
Asn	Leu	Glu	Ile	Lys	Ser	Ile	Lys	Cys							
		515					520								

<210> 369
 <211> 177
 <212> PRT
 <213> E. Coli

<400> 369

Met	Asn	Thr	Lys	Ile	Arg	Tyr	Gly	Leu	Ser	Ala	Ala	Val	Leu	Ala	Leu
1				5					10					15	
Ile	Gly	Ala	Gly	Ala	Ser	Ala	Pro	Gln	Ile	Leu	Asp	Gln	Phe	Leu	Asp
			20					25					30		
Glu	Lys	Glu	Gly	Asn	His	Thr	Met	Ala	Tyr	Arg	Asp	Gly	Ser	Gly	Ile
		35					40					45			
Trp	Thr	Ile	Cys	Arg	Gly	Ala	Thr	Val	Val	Asp	Gly	Lys	Thr	Val	Phe
	50					55					60				
Pro	Asn	Met	Lys	Leu	Ser	Lys	Glu	Lys	Cys	Asp	Gln	Val	Asn	Ala	Ile
65					70					75					80
Glu	Arg	Asp	Lys	Ala	Leu	Ala	Trp	Val	Glu	Arg	Asn	Ile	Lys	Val	Pro
				85					90					95	

Leu	Thr	Glu	Pro	Gln	Lys	Ala	Gly	Ile	Ala	Ser	Phe	Cys	Pro	Tyr	Asn	
			100					105					110			
Ile	Gly	Pro	Gly	Lys	Cys	Phe	Pro	Ser	Thr	Phe	Tyr	Lys	Arg	Leu	Asn	
		115					120					125				
Ala	Gly	Asp	Arg	Lys	Gly	Ala	Cys	Glu	Ala	Ile	Arg	Trp	Trp	Ile	Lys	
	130				135						140					
Asp	Gly	Gly	Arg	Asp	Cys	Arg	Ile	Arg	Ser	Asn	Asn	Cys	Tyr	Gly	Gln	
145					150					155					160	
Val	Ile	Arg	Arg	Asp	Gln	Glu	Ser	Ala	Leu	Thr	Cys	Trp	Gly	Ile	Glu	
				165					170					175		

Gln

<210> 370
 <211> 103
 <212> PRT
 <213> E. Coli

<400> 370

Met	Thr	Gln	Asp	Tyr	Glu	Leu	Val	Val	Lys	Gly	Val	Arg	Asn	Phe	Glu	
1			5						10					15		
Asn	Lys	Val	Thr	Val	Thr	Val	Ala	Leu	Gln	Asp	Lys	Glu	Arg	Phe	Asp	
		20						25					30			
Gly	Glu	Ile	Phe	Asp	Leu	Asp	Val	Ala	Met	Asp	Arg	Val	Glu	Gly	Ala	
	35						40					45				
Ala	Leu	Glu	Phe	Tyr	Glu	Ala	Ala	Ala	Arg	Arg	Ser	Val	Arg	Gln	Val	
	50					55					60					
Phe	Leu	Glu	Val	Ala	Glu	Lys	Leu	Ser	Glu	Lys	Val	Glu	Ser	Tyr	Leu	
65					70					75					80	
Gln	His	Gln	Tyr	Ser	Phe	Lys	Ile	Glu	Asn	Pro	Ala	Asn	Lys	His	Glu	
				85					90					95		
Arg	Pro	His	His	Lys	Tyr	Leu										
			100													

<210> 371
 <211> 96
 <212> PRT
 <213> E. Coli

<400> 371

Met	Leu	Ser	Lys	Leu	Pro	Arg	Arg	Leu	Arg	Ser	Phe	Gln	Thr	Tyr	Cys	
1			5						10					15		
Thr	Ile	Arg	Val	His	Arg	Gly	Glu	Asp	Met	Lys	Ser	Met	Asp	Lys	Leu	
			20					25					30			
Thr	Thr	Gly	Val	Ala	Tyr	Gly	Thr	Ser	Ala	Gly	Asn	Ala	Gly	Phe	Trp	
	35						40					45				
Ala	Leu	Gln	Leu	Leu	Asp	Lys	Val	Thr	Pro	Ser	Gln	Trp	Ala	Ala	Ile	
	50					55					60					
Gly	Val	Leu	Gly	Ser	Leu	Val	Phe	Gly	Leu	Leu	Thr	Tyr	Leu	Thr	Asn	
65					70					75					80	
Leu	Tyr	Phe	Lys	Ile	Lys	Glu	Asp	Arg	Arg	Lys	Ala	Ala	Arg	Gly	Glu	
				85					90					95		

<210> 372
 <211> 71
 <212> PRT
 <213> E. Coli

<400> 372
 Met Ser Asn Lys Met Thr Gly Leu Val Lys Trp Phe Asn Ala Asp Lys
 1 5 10 15
 Gly Phe Gly Phe Ile Ser Pro Val Asp Gly Ser Lys Asp Val Phe Val
 20 25 30
 His Phe Ser Ala Ile Gln Asn Asp Asn Tyr Arg Thr Leu Phe Glu Gly
 35 40 45
 Gln Lys Val Thr Phe Ser Ile Glu Ser Gly Ala Lys Gly Pro Ala Ala
 50 55 60
 Ala Asn Val Ile Ile Thr Asp
 65 70

<210> 373
 <211> 338
 <212> PRT
 <213> E. Coli

<400> 373
 Met Phe Val Ile Trp Ser His Arg Thr Gly Phe Ile Met Ser His Gln
 1 5 10 15
 Leu Thr Phe Ala Asp Ser Glu Phe Ser Lys Arg Arg Gln Thr Arg
 20 25 30
 Lys Glu Ile Phe Leu Ser Arg Met Glu Gln Ile Leu Pro Trp Gln Asn
 35 40 45
 Met Val Glu Val Ile Glu Pro Phe Tyr Pro Lys Ala Gly Asn Gly Arg
 50 55 60
 Arg Pro Tyr Pro Leu Glu Thr Met Leu Arg Ile His Cys Met Gln His
 65 70 75 80
 Trp Tyr Asn Leu Ser Asp Gly Ala Met Glu Asp Ala Leu Tyr Glu Ile
 85 90 95
 Ala Ser Met Arg Leu Phe Ala Arg Leu Ser Leu Asp Ser Ala Leu Pro
 100 105 110
 Asp Arg Thr Thr Ile Met Asn Phe Arg His Leu Leu Glu Gln His Gln
 115 120 125
 Leu Ala Arg Gln Leu Phe Lys Thr Ile Asn Arg Trp Leu Ala Glu Ala
 130 135 140
 Gly Val Met Met Thr Gln Gly Thr Leu Val Asp Ala Thr Ile Ile Glu
 145 150 155 160
 Ala Pro Ser Ser Thr Lys Asn Lys Glu Gln Gln Arg Asp Pro Glu Met
 165 170 175
 His Gln Thr Lys Lys Gly Asn Gln Trp His Phe Gly Met Lys Ala His
 180 185 190
 Ile Gly Val Asp Ala Lys Ser Gly Leu Thr His Ser Leu Val Thr Thr
 195 200 205
 Ala Ala Asn Glu His Asp Leu Asn Gln Leu Gly Asn Leu Leu His Gly
 210 215 220
 Glu Glu Gln Phe Val Ser Ala Asp Ala Gly Tyr Gln Gly Ala Pro Gln
 225 230 235 240
 Arg Glu Glu Leu Ala Glu Val Asp Val Asp Trp Leu Ile Ala Glu Arg

				245					250					255			
Pro	Gly	Lys	Val	Arg	Thr	Leu	Lys	Gln	His	Pro	Arg	Lys	Asn	Lys	Thr		
			260					265					270				
Ala	Ile	Asn	Ile	Glu	Tyr	Met	Lys	Ala	Ser	Ile	Arg	Ala	Arg	Val	Glu		
		275					280					285					
His	Pro	Phe	Arg	Ile	Ile	Lys	Arg	Gln	Phe	Gly	Phe	Val	Lys	Ala	Arg		
	290					295					300						
Tyr	Lys	Gly	Leu	Leu	Lys	Asn	Asp	Asn	Gln	Leu	Ala	Met	Leu	Phe	Thr		
305					310					315					320		
Leu	Ala	Asn	Leu	Phe	Arg	Ala	Asp	Gln	Met	Ile	Arg	Gln	Trp	Glu	Arg		
			325					330						335			
Ser	His																

<210> 374
 <211> 157
 <212> PRT
 <213> E. Coli

Met	Val	Tyr	Ile	Ile	Ile	Val	Ser	His	Gly	His	Glu	Asp	Tyr	Ile	Lys		
1			5						10					15			
Lys	Leu	Leu	Glu	Asn	Leu	Asn	Ala	Asp	Asp	Glu	His	Tyr	Lys	Ile	Ile		
		20						25					30				
Val	Arg	Asp	Asn	Lys	Asp	Ser	Leu	Leu	Lys	Gln	Ile	Cys	Gln	His			
		35				40						45					
Tyr	Ala	Gly	Leu	Asp	Tyr	Ile	Ser	Gly	Gly	Val	Tyr	Gly	Phe	Gly	His		
	50					55					60						
Asn	Asn	Asn	Ile	Ala	Val	Ala	Tyr	Val	Lys	Glu	Lys	Tyr	Arg	Pro	Ala		
65				70						75					80		
Asp	Asp	Asp	Tyr	Ile	Leu	Phe	Leu	Asn	Pro	Asp	Ile	Ile	Met	Lys	His		
			85						90					95			
Asp	Asp	Leu	Leu	Thr	Tyr	Ile	Lys	Tyr	Val	Glu	Ser	Lys	Arg	Tyr	Ala		
		100						105					110				
Phe	Ser	Thr	Leu	Cys	Leu	Phe	Arg	Asp	Glu	Ala	Lys	Ser	Leu	His	Asp		
		115					120						125				
Tyr	Ser	Val	Arg	Lys	Phe	Pro	Val	Leu	Ser	Asp	Phe	Ile	Val	Ser	Phe		
	130					135					140						
Met	Leu	Gly	Ile	Lys	Glu	Gly	Ala	Asn	Lys	Ser	Leu	Ile					
145					150					155							

<210> 375
 <211> 372
 <212> PRT
 <213> E. Coli

Met	Gly	Lys	Ser	Ile	Val	Val	Val	Ser	Ala	Val	Asn	Phe	Thr	Thr	Gly		
1			5						10					15			
Gly	Pro	Phe	Thr	Ile	Leu	Lys	Lys	Phe	Leu	Ala	Ala	Thr	Asn	Asn	Lys		
		20						25					30				
Glu	Asn	Val	Ser	Phe	Ile	Ala	Leu	Val	His	Ser	Ala	Lys	Glu	Leu	Lys		
		35					40					45					
Glu	Ser	Tyr	Pro	Trp	Val	Lys	Phe	Ile	Glu	Phe	Pro	Glu	Val	Lys	Gly		

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Ser	Trp	Leu	Lys	Arg	Leu	His	Phe	Glu	Tyr	Val	Val	Cys	Lys	Lys	Leu
65					70					75					80
Ser	Lys	Glu	Leu	Asn	Ala	Thr	His	Trp	Ile	Cys	Leu	His	Asp	Ile	Thr
				85					90					95	
Ala	Asn	Val	Val	Thr	Lys	Lys	Arg	Tyr	Val	Tyr	Cys	His	Asn	Pro	Ala
			100					105					110		
Pro	Phe	Tyr	Lys	Gly	Ile	Leu	Phe	Arg	Glu	Ile	Leu	Met	Glu	Pro	Ser
		115					120					125			
Phe	Phe	Leu	Phe	Lys	Met	Leu	Tyr	Gly	Leu	Ile	Tyr	Lys	Ile	Asn	Ile
	130					135					140				
Lys	Lys	Asn	Thr	Ala	Val	Phe	Val	Gln	Gln	Phe	Trp	Met	Lys	Glu	Lys
145				150						155					160
Phe	Ile	Lys	Lys	Tyr	Ser	Ile	Asn	Asn	Ile	Ile	Val	Ser	Arg	Pro	Glu
				165					170					175	
Ile	Lys	Leu	Ser	Asp	Lys	Ser	Gln	Leu	Thr	Asp	Asp	Asp	Ser	Gln	Phe
			180					185					190		
Lys	Asn	Asn	Pro	Ser	Glu	Leu	Thr	Ile	Phe	Tyr	Pro	Ala	Val	Pro	Arg
		195					200					205			
Val	Phe	Lys	Asn	Tyr	Glu	Leu	Ile	Ile	Ser	Ala	Ala	Arg	Lys	Leu	Lys
	210					215						220			
Glu	Gln	Ser	Asn	Ile	Lys	Phe	Leu	Leu	Thr	Ile	Ser	Gly	Thr	Glu	Asn
225				230						235					240
Ala	Tyr	Ala	Lys	Tyr	Ile	Ile	Ser	Leu	Ala	Glu	Gly	Leu	Asp	Asn	Val
				245					250					255	
His	Phe	Leu	Gly	Tyr	Leu	Asp	Lys	Glu	Lys	Ile	Asp	His	Cys	Tyr	Asn
			260					265					270		
Ile	Ser	Asp	Ile	Val	Cys	Phe	Pro	Ser	Arg	Leu	Glu	Thr	Trp	Gly	Leu
		275					280						285		
Pro	Leu	Ser	Glu	Ala	Lys	Glu	Arg	Gly	Lys	Trp	Val	Leu	Ala	Ser	Asp
	290					295					300				
Phe	Pro	Phe	Thr	Arg	Glu	Thr	Leu	Gly	Ser	Tyr	Glu	Lys	Lys	Ala	Phe
305				310						315					320
Phe	Asp	Ser	Asn	Asn	Asp	Asp	Met	Leu	Val	Lys	Leu	Ile	Ile	Asp	Phe
				325					330					335	
Lys	Lys	Gly	Asn	Leu	Lys	Lys	Asp	Ile	Ser	Asp	Ala	Asn	Phe	Ile	Tyr
			340					345					350		
Arg	Asn	Glu	Asn	Val	Leu	Val	Gly	Phe	Asp	Glu	Leu	Val	Asn	Phe	Ile
		355					360					365			
Thr	Glu	Glu	His												
			370												

<210> 376
 <211> 196
 <212> PRT
 <213> E. Coli

<400> 376															
Met	Ile	Leu	Lys	Leu	Ala	Lys	Arg	Tyr	Gly	Leu	Cys	Gly	Phe	Ile	Arg
1				5					10					15	
Leu	Val	Arg	Asp	Val	Leu	Leu	Thr	Arg	Val	Phe	Tyr	Arg	Asn	Cys	Arg
			20					25					30		
Ile	Ile	Arg	Phe	Pro	Cys	Tyr	Ile	Arg	Asn	Asp	Gly	Ser	Ile	Asn	Phe
		35					40					45			
Gly	Glu	Asn	Phe	Thr	Ser	Gly	Val	Gly	Leu	Arg	Leu	Asp	Ala	Phe	Gly
	50					55					60				

Arg	Gly	Val	Ile	Phe	Phe	Ser	Asp	Asn	Val	Gln	Val	Asn	Asp	Tyr	Val
65					70					75					80
His	Ile	Ala	Ser	Ile	Glu	Ser	Val	Thr	Ile	Gly	Arg	Asp	Thr	Leu	Ile
				85					90					95	
Ala	Ser	Lys	Val	Phe	Ile	Thr	Asp	His	Asn	His	Gly	Ser	Phe	Lys	His
			100					105					110		
Ser	Asp	Pro	Met	Ser	Ser	Pro	Asn	Ile	Pro	Pro	Asp	Met	Arg	Thr	Leu
		115					120					125			
Glu	Ser	Ser	Ala	Val	Val	Ile	Gly	Gln	Arg	Val	Trp	Leu	Gly	Glu	Asn
	130					135					140				
Val	Thr	Val	Leu	Pro	Gly	Thr	Ile	Ile	Gly	Asn	Gly	Val	Val	Val	Gly
145					150					155					160
Ala	Asn	Ser	Val	Val	Arg	Gly	Ser	Ile	Pro	Glu	Asn	Thr	Val	Ile	Ala
				165					170					175	
Gly	Val	Pro	Ala	Lys	Ile	Ile	Lys	Lys	Tyr	Asn	His	Glu	Thr	Lys	Leu
			180					185					190		
Trp	Glu	Lys	Ala												
			195												

<210> 377
 <211> 330
 <212> PRT
 <213> E. Coli

<400> 377															
Met	Tyr	Phe	Leu	Asn	Asp	Leu	Asn	Phe	Ser	Arg	Arg	Asp	Ala	Gly	Phe
1				5					10					15	
Lys	Ala	Arg	Lys	Asp	Ala	Leu	Asp	Ile	Ala	Ser	Asp	Tyr	Glu	Asn	Ile
			20					25					30		
Ser	Val	Val	Asn	Ile	Pro	Leu	Trp	Gly	Gly	Val	Val	Gln	Arg	Ile	Ile
			35				40					45			
Ser	Ser	Val	Lys	Leu	Ser	Thr	Phe	Leu	Cys	Gly	Leu	Glu	Asn	Lys	Asp
	50					55					60				
Val	Leu	Ile	Phe	Asn	Phe	Pro	Met	Ala	Lys	Pro	Phe	Trp	His	Ile	Leu
65					70					75					80
Ser	Phe	Phe	His	Arg	Leu	Leu	Lys	Phe	Arg	Ile	Val	Pro	Leu	Ile	His
				85					90					95	
Asp	Ile	Asp	Glu	Leu	Arg	Gly	Gly	Gly	Gly	Ser	Asp	Ser	Val	Arg	Leu
			100					105					110		
Ala	Thr	Cys	Asp	Met	Val	Ile	Ser	His	Asn	Pro	Gln	Met	Thr	Lys	Tyr
		115					120					125			
Leu	Ser	Lys	Tyr	Met	Ser	Gln	Asp	Lys	Ile	Lys	Asp	Ile	Lys	Ile	Phe
	130					135					140				
Asp	Tyr	Leu	Val	Ser	Ser	Asp	Val	Glu	His	Arg	Asp	Val	Thr	Asp	Lys
145					150					155					160
Gln	Arg	Gly	Val	Ile	Tyr	Ala	Gly	Asn	Leu	Ser	Arg	His	Lys	Cys	Ser
				165					170					175	
Phe	Ile	Tyr	Thr	Glu	Gly	Cys	Asp	Phe	Thr	Leu	Phe	Gly	Val	Asn	Tyr
			180					185					190		
Glu	Asn	Lys	Asp	Asn	Pro	Lys	Tyr	Leu	Gly	Ser	Phe	Asp	Ala	Gln	Ser
		195					200					205			
Pro	Glu	Lys	Ile	Asn	Leu	Pro	Gly	Met	Gln	Phe	Gly	Leu	Ile	Trp	Asp
	210					215						220			
Gly	Asp	Ser	Val	Glu	Thr	Cys	Ser	Gly	Ala	Phe	Gly	Asp	Tyr	Leu	Lys
225					230					235					240
Phe	Asn	Asn	Pro	His	Lys	Thr	Ser	Leu	Tyr	Leu	Ser	Met	Glu	Leu	Pro
				245					250					255	

Val	Phe	Ile	Trp	Asp	Lys	Ala	Ala	Leu	Ala	Asp	Phe	Ile	Val	Asp	Asn
			260					265					270		
Arg	Ile	Gly	Tyr	Ala	Val	Gly	Ser	Ile	Lys	Glu	Met	Gln	Glu	Ile	Val
		275					280					285			
Asp	Ser	Met	Thr	Ile	Glu	Thr	Tyr	Lys	Gln	Ile	Ser	Glu	Asn	Thr	Lys
	290					295					300				
Ile	Ile	Ser	Gln	Lys	Ile	Arg	Thr	Gly	Ser	Tyr	Phe	Arg	Asp	Val	Leu
305					310					315					320
Glu	Glu	Val	Ile	Asp	Asp	Leu	Lys	Thr	Arg						
			325					330							

<210> 378
 <211> 388
 <212> PRT
 <213> E. Coli

<400> 378															
Met	Ile	Tyr	Leu	Val	Ile	Ser	Val	Phe	Leu	Ile	Thr	Ala	Phe	Ile	Cys
1				5					10					15	
Leu	Tyr	Leu	Lys	Lys	Asp	Ile	Phe	Tyr	Pro	Ala	Val	Cys	Val	Asn	Ile
			20					25					30		
Ile	Phe	Ala	Leu	Val	Leu	Leu	Gly	Tyr	Glu	Ile	Thr	Ser	Asp	Ile	Tyr
		35					40					45			
Ala	Phe	Gln	Leu	Asn	Asp	Ala	Thr	Leu	Ile	Phe	Leu	Leu	Cys	Asn	Val
	50					55					60				
Leu	Thr	Phe	Thr	Leu	Ser	Cys	Leu	Leu	Thr	Glu	Ser	Val	Leu	Asp	Leu
65					70					75					80
Asn	Ile	Arg	Lys	Val	Asn	Asn	Ala	Ile	Tyr	Ser	Ile	Pro	Ser	Lys	Lys
				85					90					95	
Val	His	Asn	Val	Gly	Leu	Leu	Val	Ile	Ser	Phe	Ser	Met	Ile	Tyr	Ile
			100					105						110	
Cys	Met	Arg	Leu	Ser	Asn	Tyr	Gln	Phe	Gly	Thr	Ser	Leu	Leu	Ser	Tyr
		115					120					125			
Met	Asn	Leu	Ile	Arg	Asp	Ala	Asp	Val	Glu	Asp	Thr	Ser	Arg	Asn	Phe
	130					135					140				
Ser	Ala	Tyr	Met	Gln	Pro	Ile	Ile	Leu	Thr	Thr	Phe	Ala	Leu	Phe	Ile
145					150					155					160
Trp	Ser	Lys	Lys	Phe	Thr	Asn	Thr	Lys	Val	Ser	Lys	Thr	Phe	Thr	Leu
			165						170					175	
Leu	Val	Phe	Ile	Val	Phe	Ile	Phe	Ala	Ile	Ile	Leu	Asn	Thr	Gly	Lys
		180						185					190		
Gln	Ile	Val	Phe	Met	Val	Ile	Ile	Ser	Tyr	Ala	Phe	Ile	Val	Gly	Val
	195						200					205			
Asn	Arg	Val	Lys	His	Tyr	Val	Tyr	Leu	Ile	Thr	Ala	Val	Gly	Val	Leu
	210					215					220				
Phe	Ser	Leu	Tyr	Met	Leu	Phe	Leu	Arg	Gly	Leu	Pro	Gly	Gly	Met	Ala
225					230					235					240
Tyr	Tyr	Leu	Ser	Met	Tyr	Leu	Val	Ser	Pro	Ile	Ile	Ala	Phe	Gln	Glu
			245						250					255	
Phe	Tyr	Phe	Gln	Gln	Val	Ser	Asn	Ser	Ala	Ser	Ser	His	Val	Phe	Trp
		260						265					270		
Phe	Phe	Glu	Arg	Leu	Met	Gly	Leu	Leu	Thr	Gly	Gly	Val	Ser	Met	Ser
		275					280					285			
Leu	His	Lys	Glu	Phe	Val	Trp	Val	Gly	Leu	Pro	Thr	Asn	Val	Tyr	Thr
	290					295					300				
Ala	Phe	Ser	Asp	Tyr	Val	Tyr	Ile	Ser	Ala	Glu	Leu	Ser	Tyr	Leu	Met

305					310					315				320
Met	Val	Ile	His	Gly	Cys	Ile	Ser	Gly	Val	Leu	Trp	Arg	Leu	Ser
				325					330					335
Asn	Tyr	Ile	Ser	Val	Lys	Ile	Phe	Tyr	Ser	Tyr	Phe	Ile	Tyr	Thr
			340					345					350	
Ser	Phe	Ile	Phe	Tyr	His	Glu	Ser	Phe	Met	Thr	Asn	Ile	Ser	Ser
		355					360					365		
Ile	Gln	Ile	Thr	Leu	Cys	Ile	Ile	Val	Phe	Ser	Gln	Phe	Leu	Lys
	370					375					380			
Gln	Lys	Ile	Lys											
385														

<210> 379
 <211> 367
 <212> PRT
 <213> E. Coli

<400> 379

Met	Tyr	Asp	Tyr	Ile	Ile	Val	Gly	Ser	Gly	Leu	Phe	Gly	Ala	Val	Cys
1				5					10					15	
Ala	Asn	Glu	Leu	Lys	Lys	Leu	Asn	Lys	Lys	Val	Leu	Val	Ile	Glu	Lys
			20					25					30		
Arg	Asn	His	Ile	Gly	Gly	Asn	Ala	Tyr	Thr	Glu	Asp	Cys	Glu	Gly	Ile
		35				40						45			
Gln	Ile	His	Lys	Tyr	Gly	Ala	His	Ile	Phe	His	Thr	Asn	Asp	Lys	Tyr
	50					55					60				
Ile	Trp	Asp	Tyr	Val	Asn	Asp	Leu	Val	Glu	Phe	Asn	Arg	Phe	Thr	Asn
					70				75					80	
Ser	Pro	Leu	Ala	Ile	Tyr	Lys	Asp	Lys	Leu	Phe	Asn	Leu	Pro	Phe	Asn
				85					90					95	
Met	Asn	Thr	Phe	His	Gln	Met	Trp	Gly	Val	Lys	Asp	Pro	Gln	Glu	Ala
			100					105					110		
Gln	Asn	Ile	Ile	Asn	Ala	Gln	Lys	Lys	Lys	Tyr	Gly	Asp	Lys	Val	Pro
		115					120					125			
Glu	Asn	Leu	Glu	Glu	Gln	Ala	Ile	Ser	Leu	Val	Gly	Glu	Asp	Leu	Tyr
	130					135					140				
Gln	Ala	Leu	Ile	Lys	Gly	Tyr	Thr	Glu	Lys	Gln	Trp	Gly	Arg	Ser	Ala
	145				150				155					160	
Lys	Glu	Leu	Pro	Ala	Phe	Ile	Ile	Lys	Arg	Ile	Pro	Val	Arg	Phe	Thr
				165					170					175	
Phe	Asp	Asn	Asn	Tyr	Phe	Ser	Asp	Arg	Tyr	Gln	Gly	Ile	Pro	Val	Gly
		180						185					190		
Gly	Tyr	Thr	Lys	Leu	Ile	Glu	Lys	Met	Leu	Glu	Gly	Val	Asp	Val	Lys
	195						200					205			
Leu	Gly	Ile	Asp	Phe	Leu	Lys	Asp	Lys	Asp	Ser	Leu	Ala	Ser	Lys	Ala
	210					215					220				
His	Arg	Ile	Ile	Tyr	Thr	Gly	Pro	Ile	Asp	Gln	Tyr	Phe	Asp	Tyr	Arg
	225				230					235				240	
Phe	Gly	Ala	Leu	Glu	Tyr	Arg	Ser	Leu	Lys	Phe	Glu	Thr	Glu	Arg	His
				245					250					255	
Glu	Phe	Pro	Asn	Phe	Gln	Gly	Asn	Ala	Val	Ile	Asn	Phe	Thr	Asp	Ala
			260					265					270		
Asn	Val	Pro	Tyr	Thr	Arg	Ile	Ile	Glu	His	Lys	His	Phe	Asp	Tyr	Val
		275					280					285			
Glu	Thr	Lys	His	Thr	Val	Val	Thr	Lys	Glu	Tyr	Pro	Leu	Glu	Trp	Lys

290		295		300
Val Gly Asp Glu Pro Tyr	Tyr Pro Val Asn Asp	Asn Lys Asn Met Glu		
305	310	315	320	
Leu Phe Lys Lys Tyr Arg	Glu Leu Ala Ser Arg	Glu Asp Lys Val Ile		
	325	330	335	
Phe Gly Gly Arg Leu Ala	Glu Tyr Lys Tyr Asp	Met His Gln Val		
	340	345	350	
Ile Ser Ala Ala Leu Tyr	Gln Val Lys Asn Ile Met	Ser Thr Asp		
	355	360	365	

<210> 380
 <211> 371
 <212> PRT
 <213> E. Coli

<400> 380	
Met Phe Pro Lys Ile Met Asn Asp Glu Asn Phe Phe Lys Lys Ala Ala	
1 5 10 15	
Ala His Gly Glu Glu Pro Pro Leu Thr Pro Gln Asn Glu His Gln Arg	
20 25 30	
Ser Gly Leu Arg Phe Ala Arg Arg Val Arg Leu Pro Arg Ala Val Gly	
35 40 45	
Leu Ala Gly Met Phe Leu Pro Ile Ala Ser Thr Leu Val Ser His Pro	
50 55 60	
Pro Pro Gly Trp Trp Trp Leu Val Leu Val Gly Trp Ala Phe Val Trp	
65 70 75 80	
Pro His Leu Ala Trp Gln Ile Ala Ser Arg Ala Val Asp Pro Leu Ser	
85 90 95	
Arg Glu Ile Tyr Asn Leu Lys Thr Asp Ala Val Leu Ala Gly Met Trp	
100 105 110	
Val Gly Val Met Gly Val Asn Val Leu Pro Ser Thr Ala Met Leu Met	
115 120 125	
Ile Met Cys Leu Asn Leu Met Gly Ala Gly Gly Pro Arg Leu Phe Val	
130 135 140	
Ala Gly Leu Val Leu Met Val Val Ser Cys Leu Val Thr Leu Glu Leu	
145 150 155 160	
Thr Gly Ile Thr Val Ser Phe Asn Ser Ala Pro Leu Glu Trp Trp Leu	
165 170 175	
Ser Leu Pro Ile Ile Val Ile Tyr Pro Leu Leu Phe Gly Trp Val Ser	
180 185 190	
Tyr Gln Thr Ala Thr Lys Leu Ala Glu His Lys Arg Arg Leu Gln Val	
195 200 205	
Met Ser Thr Arg Asp Gly Met Thr Gly Val Tyr Asn Arg Arg His Trp	
210 215 220	
Glu Thr Met Leu Arg Asn Glu Phe Asp Asn Cys Arg Arg His Asn Arg	
225 230 235 240	
Asp Ala Thr Leu Leu Ile Ile Asp Ile Asp His Phe Lys Ser Ile Asn	
245 250 255	
Asp Thr Trp Gly His Asp Val Gly Asp Glu Ala Ile Val Ala Leu Thr	
260 265 270	
Arg Gln Leu Gln Ile Thr Leu Arg Gly Ser Asp Val Ile Gly Arg Phe	
275 280 285	
Gly Gly Asp Glu Phe Ala Val Ile Met Ser Gly Thr Pro Ala Glu Ser	
290 295 300	
Ala Ile Thr Ala Met Leu Arg Val His Glu Gly Leu Asn Thr Leu Arg	
305 310 315 320	

<210> 383
 <211> 84
 <212> PRT
 <213> E. Coli

<400> 383

Met	Thr	Asp	Lys	Ile	Arg	Thr	Leu	Gln	Gly	Arg	Val	Val	Ser	Asp	Lys
1				5					10					15	
Met	Glu	Lys	Ser	Ile	Val	Val	Ala	Ile	Glu	Arg	Phe	Val	Lys	His	Pro
			20					25					30		
Ile	Tyr	Gly	Lys	Phe	Ile	Lys	Arg	Thr	Thr	Lys	Leu	His	Val	His	Asp
		35					40					45			
Glu	Asn	Asn	Glu	Cys	Gly	Ile	Gly	Asp	Val	Val	Glu	Ile	Arg	Glu	Cys
	50					55					60				
Arg	Pro	Leu	Ser	Lys	Thr	Lys	Ser	Trp	Thr	Leu	Val	Arg	Val	Val	Glu
65					70					75					80
Lys	Ala	Val	Leu												

<210> 384
 <211> 63
 <212> PRT
 <213> E. Coli

<400> 384

Met	Lys	Ala	Lys	Glu	Leu	Arg	Glu	Lys	Ser	Val	Glu	Glu	Leu	Asn	Thr
1				5					10					15	
Glu	Leu	Leu	Asn	Leu	Leu	Arg	Glu	Gln	Phe	Asn	Leu	Arg	Met	Gln	Ala
			20					25					30		
Ala	Ser	Gly	Gln	Leu	Gln	Gln	Ser	His	Leu	Leu	Lys	Gln	Val	Arg	Arg
		35					40					45			
Asp	Val	Ala	Arg	Val	Lys	Thr	Leu	Leu	Asn	Glu	Lys	Ala	Gly	Ala	
	50					55					60				

<210> 385
 <211> 136
 <212> PRT
 <213> E. Coli

<400> 385

Met	Leu	Gln	Pro	Lys	Arg	Thr	Lys	Phe	Arg	Lys	Met	His	Lys	Gly	Arg
1				5					10					15	
Asn	Arg	Gly	Leu	Ala	Gln	Gly	Thr	Asp	Val	Ser	Phe	Gly	Ser	Phe	Gly
		20						25					30		
Leu	Lys	Ala	Val	Gly	Arg	Gly	Arg	Leu	Thr	Ala	Arg	Gln	Ile	Glu	Ala
		35					40					45			
Ala	Arg	Arg	Ala	Met	Thr	Arg	Ala	Val	Lys	Arg	Gln	Gly	Lys	Ile	Trp
	50					55					60				
Ile	Arg	Val	Phe	Pro	Asp	Lys	Pro	Ile	Thr	Glu	Lys	Pro	Leu	Ala	Val
65					70					75					80
Arg	Met	Gly	Lys	Gly	Lys	Gly	Asn	Val	Glu	Tyr	Trp	Val	Ala	Leu	Ile
			85						90				95		
Gln	Pro	Gly	Lys	Val	Leu	Tyr	Glu	Met	Asp	Gly	Val	Pro	Glu	Glu	Leu
		100					105						110		
Ala	Arg	Glu	Ala	Phe	Lys	Leu	Ala	Ala	Ala	Lys	Leu	Pro	Ile	Lys	Thr
		115					120					125			

Thr Phe Val Thr Lys Thr Val Met
130 135

<210> 386
<211> 233
<212> PRT
<213> E. Coli

<400> 386

Met	Gly	Gln	Lys	Val	His	Pro	Asn	Gly	Ile	Arg	Leu	Gly	Ile	Val	Lys	
1				5					10					15		
Pro	Trp	Asn	Ser	Thr	Trp	Phe	Ala	Asn	Thr	Lys	Glu	Phe	Ala	Asp	Asn	
		20						25					30			
Leu	Asp	Ser	Asp	Phe	Lys	Val	Arg	Gln	Tyr	Leu	Thr	Lys	Glu	Leu	Ala	
		35					40					45				
Lys	Ala	Ser	Val	Ser	Arg	Ile	Val	Ile	Glu	Arg	Pro	Ala	Lys	Ser	Ile	
	50					55				60						
Arg	Val	Thr	Ile	His	Thr	Ala	Arg	Pro	Gly	Ile	Val	Ile	Gly	Lys	Lys	
65				70					75						80	
Gly	Glu	Asp	Val	Glu	Lys	Leu	Arg	Lys	Val	Val	Ala	Asp	Ile	Ala	Gly	
				85					90					95		
Val	Pro	Ala	Gln	Ile	Asn	Ile	Ala	Glu	Val	Arg	Lys	Pro	Glu	Leu	Asp	
		100						105					110			
Ala	Lys	Leu	Val	Ala	Asp	Ser	Ile	Thr	Ser	Gln	Leu	Glu	Arg	Arg	Val	
		115					120					125				
Met	Phe	Arg	Arg	Ala	Met	Lys	Arg	Ala	Val	Gln	Asn	Ala	Met	Arg	Leu	
	130					135				140						
Gly	Ala	Lys	Gly	Ile	Lys	Val	Glu	Val	Ser	Gly	Arg	Leu	Gly	Gly	Ala	
145				150					155						160	
Glu	Ile	Ala	Arg	Thr	Glu	Trp	Tyr	Arg	Glu	Gly	Arg	Val	Pro	Leu	His	
			165					170						175		
Thr	Leu	Arg	Ala	Asp	Ile	Asp	Tyr	Asn	Thr	Ser	Glu	Ala	His	Thr	Thr	
		180						185					190			
Tyr	Gly	Val	Ile	Gly	Val	Lys	Val	Trp	Ile	Phe	Lys	Gly	Glu	Ile	Leu	
	195					200						205				
Gly	Gly	Met	Ala	Ala	Val	Glu	Gln	Pro	Glu	Lys	Pro	Ala	Ala	Gln	Pro	
	210					215					220					
Lys	Lys	Gln	Gln	Arg	Lys	Gly	Arg	Lys								
225					230											

<210> 387
<211> 110
<212> PRT
<213> E. Coli

<400> 387

Met	Glu	Thr	Ile	Ala	Lys	His	Arg	His	Ala	Arg	Ser	Ser	Ala	Gln	Lys	
1				5					10					15		
Val	Arg	Leu	Val	Ala	Asp	Leu	Ile	Arg	Gly	Lys	Lys	Val	Ser	Gln	Ala	
		20						25					30			
Leu	Asp	Ile	Leu	Thr	Tyr	Thr	Asn	Lys	Lys	Ala	Ala	Val	Leu	Val	Lys	
		35					40					45				
Lys	Val	Leu	Glu	Ser	Ala	Ile	Ala	Asn	Ala	Glu	His	Asn	Asp	Gly	Ala	

50					55					60					
Asp	Ile	Asp	Asp	Leu	Lys	Val	Thr	Lys	Ile	Phe	Val	Asp	Glu	Gly	Pro
65					70					75					80
Ser	Met	Lys	Arg	Ile	Met	Pro	Arg	Ala	Lys	Gly	Arg	Ala	Asp	Arg	Ile
				85					90					95	
Leu	Lys	Arg	Thr	Ser	His	Ile	Thr	Val	Val	Val	Ser	Asp	Arg		
			100					105					110		

<210> 388
 <211> 92
 <212> PRT
 <213> E. Coli

<400> 388															
Met	Pro	Arg	Ser	Leu	Lys	Lys	Gly	Pro	Phe	Ile	Asp	Leu	His	Leu	Leu
1				5					10					15	
Met	Lys	Val	Glu	Lys	Ala	Val	Glu	Ser	Gly	Asp	Lys	Lys	Pro	Leu	Arg
			20					25					30		
Thr	Trp	Ser	Arg	Arg	Ser	Thr	Ile	Phe	Pro	Asn	Met	Ile	Gly	Leu	Thr
		35					40					45			
Ile	Ala	Val	His	Asn	Gly	Arg	Gln	His	Val	Pro	Val	Phe	Val	Thr	Asp
	50				55					60					
Glu	Met	Val	Gly	His	Lys	Leu	Gly	Glu	Phe	Ala	Pro	Thr	Arg	Thr	Tyr
65					70				75						80
Arg	Gly	His	Ala	Ala	Asp	Lys	Lys	Ala	Lys	Lys	Lys				
				85					90						

<210> 389
 <211> 273
 <212> PRT
 <213> E. Coli

<400> 389															
Met	Ala	Val	Val	Lys	Cys	Lys	Pro	Thr	Ser	Pro	Gly	Arg	Arg	His	Val
1				5					10					15	
Val	Lys	Val	Val	Asn	Pro	Glu	Leu	His	Lys	Gly	Lys	Pro	Phe	Ala	Pro
			20					25					30		
Leu	Leu	Glu	Lys	Asn	Ser	Lys	Ser	Gly	Gly	Arg	Asn	Asn	Asn	Gly	Arg
		35					40					45			
Ile	Thr	Thr	Arg	His	Ile	Gly	Gly	Gly	His	Lys	Gln	Ala	Tyr	Arg	Ile
	50				55						60				
Val	Asp	Phe	Lys	Arg	Asn	Lys	Asp	Gly	Ile	Pro	Ala	Val	Val	Glu	Arg
65					70				75						80
Leu	Glu	Tyr	Asp	Pro	Asn	Arg	Ser	Ala	Asn	Ile	Ala	Leu	Val	Leu	Tyr
				85					90					95	
Lys	Asp	Gly	Glu	Arg	Arg	Tyr	Ile	Leu	Ala	Pro	Lys	Gly	Leu	Lys	Ala
		100						105					110		
Gly	Asp	Gln	Ile	Gln	Ser	Gly	Val	Asp	Ala	Ala	Ile	Lys	Pro	Gly	Asn
		115					120					125			
Thr	Leu	Pro	Met	Arg	Asn	Ile	Pro	Val	Gly	Ser	Thr	Val	His	Asn	Val
	130					135					140				
Glu	Met	Lys	Pro	Gly	Lys	Gly	Gly	Gln	Leu	Ala	Arg	Ser	Ala	Gly	Thr
145					150				155						160

Tyr Val Gln Ile Val Ala Arg Asp Gly Ala Tyr Val Thr Leu Arg Leu
 165 170 175
 Arg Ser Gly Glu Met Arg Lys Val Glu Ala Asp Cys Arg Ala Thr Leu
 180 185 190
 Gly Glu Val Gly Asn Ala Glu His Met Leu Arg Val Leu Gly Lys Ala
 195 200 205
 Gly Ala Ala Arg Trp Arg Gly Val Arg Pro Thr Val Arg Gly Thr Ala
 210 215 220
 Met Asn Pro Val Asp His Pro His Gly Gly Gly Glu Gly Arg Asn Phe
 225 230 235 240
 Gly Lys His Pro Val Thr Pro Trp Gly Val Gln Thr Lys Gly Lys Lys
 245 250 255
 Thr Arg Ser Asn Lys Arg Thr Asp Lys Phe Ile Val Arg Arg Arg Ser
 260 265 270
 Lys

<210> 390
 <211> 100
 <212> PRT
 <213> E. Coli

<400> 390
 Met Ile Arg Glu Glu Arg Leu Leu Lys Val Leu Arg Ala Pro His Val
 1 5 10 15
 Ser Glu Lys Ala Ser Thr Ala Met Glu Lys Ser Asn Thr Ile Val Leu
 20 25 30
 Lys Val Ala Lys Asp Ala Thr Lys Ala Glu Ile Lys Ala Ala Val Gln
 35 40 45
 Lys Leu Phe Glu Val Glu Val Glu Val Val Asn Thr Leu Val Val Lys
 50 55 60
 Gly Lys Val Lys Arg His Gly Gln Arg Ile Gly Arg Arg Ser Asp Trp
 65 70 75 80
 Lys Lys Ala Tyr Val Thr Leu Lys Glu Gly Gln Asn Leu Asp Phe Val
 85 90 95
 Gly Gly Ala Glu
 100

<210> 391
 <211> 201
 <212> PRT
 <213> E. Coli

<400> 391
 Met Glu Leu Val Leu Lys Asp Ala Gln Ser Ala Leu Thr Val Ser Glu
 1 5 10 15
 Thr Thr Phe Gly Arg Asp Phe Asn Glu Ala Leu Val His Gln Val Val
 20 25 30
 Val Ala Tyr Ala Ala Gly Ala Arg Gln Gly Thr Arg Ala Gln Lys Thr
 35 40 45
 Arg Ala Glu Val Thr Gly Ser Gly Lys Lys Pro Trp Arg Gln Lys Gly
 50 55 60
 Thr Gly Arg Ala Arg Ser Gly Ser Ile Lys Ser Pro Ile Trp Arg Ser

65					70					75				80
Gly	Gly	Val	Thr	Phe	Ala	Ala	Arg	Pro	Gln	Asp	His	Ser	Gln	Lys
				85					90				95	
Asn	Lys	Lys	Met	Tyr	Arg	Gly	Ala	Leu	Lys	Ser	Ile	Leu	Ser	Glu
			100					105					110	
Val	Arg	Gln	Asp	Arg	Leu	Ile	Val	Val	Glu	Lys	Phe	Ser	Val	Glu
		115					120					125		Ala
Pro	Lys	Thr	Lys	Leu	Leu	Ala	Gln	Lys	Leu	Lys	Asp	Met	Ala	Leu
		130				135					140			Glu
Asp	Val	Leu	Ile	Ile	Thr	Gly	Glu	Leu	Asp	Glu	Asn	Leu	Phe	Leu
145				150					155					160
Ala	Arg	Asn	Leu	His	Lys	Val	Asp	Val	Arg	Asp	Ala	Thr	Gly	Ile
			165					170					175	Asp
Pro	Val	Ser	Leu	Ile	Ala	Phe	Asp	Lys	Val	Val	Met	Thr	Ala	Asp
		180					185						190	Ala
Val	Lys	Gln	Val	Glu	Glu	Met	Leu	Ala						
		195					200							

<210> 392
 <211> 209
 <212> PRT
 <213> E. Coli

<400> 392

Met	Ile	Gly	Leu	Val	Gly	Lys	Lys	Val	Gly	Met	Thr	Arg	Ile	Phe	Thr
1				5					10					15	
Glu	Asp	Gly	Val	Ser	Ile	Pro	Val	Thr	Val	Ile	Glu	Val	Glu	Ala	Asn
			20					25					30		
Arg	Val	Thr	Gln	Val	Lys	Asp	Leu	Ala	Asn	Asp	Gly	Tyr	Arg	Ala	Ile
		35					40					45			
Gln	Val	Thr	Thr	Gly	Ala	Lys	Lys	Ala	Asn	Arg	Val	Thr	Lys	Pro	Glu
	50					55				60					
Ala	Gly	His	Phe	Ala	Lys	Ala	Gly	Val	Glu	Ala	Gly	Arg	Gly	Leu	Trp
65				70					75					80	
Glu	Phe	Arg	Leu	Ala	Glu	Gly	Glu	Glu	Phe	Thr	Val	Gly	Gln	Ser	Ile
			85						90				95		
Ser	Val	Glu	Leu	Phe	Ala	Asp	Val	Lys	Lys	Val	Asp	Val	Thr	Gly	Thr
		100					105					110			
Ser	Lys	Gly	Lys	Gly	Phe	Ala	Gly	Thr	Val	Lys	Arg	Trp	Asn	Phe	Arg
	115						120					125			
Thr	Gln	Asp	Ala	Thr	His	Gly	Asn	Ser	Leu	Ser	His	Arg	Val	Pro	Gly
	130					135					140				
Ser	Ile	Gly	Gln	Asn	Gln	Thr	Pro	Gly	Lys	Val	Phe	Lys	Gly	Lys	Lys
145				150						155					160
Met	Ala	Gly	Gln	Met	Gly	Asn	Glu	Arg	Val	Thr	Val	Gln	Ser	Leu	Asp
			165					170					175		
Val	Val	Arg	Val	Asp	Ala	Glu	Arg	Asn	Leu	Leu	Leu	Val	Lys	Gly	Ala
		180						185					190		
Val	Pro	Gly	Ala	Thr	Gly	Ser	Asp	Leu	Ile	Val	Lys	Pro	Ala	Val	Lys
		195					200					205			

Ala

<210> 393
 <211> 103
 <212> PRT
 <213> E. Coli

<400> 393
 Met Gln Asn Gln Arg Ile Arg Ile Arg Leu Lys Ala Phe Asp His Arg
 1 5 10 15
 Leu Ile Asp Gln Ala Thr Ala Glu Ile Val Glu Thr Ala Lys Arg Thr
 20 25 30
 Gly Ala Gln Val Arg Gly Pro Ile Pro Leu Pro Thr Arg Lys Glu Arg
 35 40 45
 Phe Thr Val Leu Ile Ser Pro His Val Asn Lys Asp Ala Arg Asp Gln
 50 55 60
 Tyr Glu Ile Arg Thr His Leu Arg Leu Val Asp Ile Val Glu Pro Thr
 65 70 75 80
 Glu Lys Thr Val Asp Ala Leu Met Arg Leu Asp Leu Ala Ala Gly Val
 85 90 95
 Asp Val Gln Ile Ser Leu Gly
 100

<210> 394
 <211> 118
 <212> PRT
 <213> E. Coli

<400> 394
 Met Ala Arg Val Lys Arg Gly Val Ile Ala Arg Ala Arg His Lys Lys
 1 5 10 15
 Ile Leu Lys Gln Ala Lys Gly Tyr Tyr Gly Ala Arg Ser Arg Val Tyr
 20 25 30
 Arg Val Ala Phe Gln Ala Val Ile Lys Ala Gly Gln Tyr Ala Tyr Arg
 35 40 45
 Asp Arg Arg Gln Arg Lys Arg Gln Phe Arg Gln Leu Trp Ile Ala Arg
 50 55 60
 Ile Asn Ala Ala Ala Arg Gln Asn Gly Ile Ser Tyr Ser Lys Phe Ile
 65 70 75 80
 Asn Gly Leu Lys Lys Ala Ser Val Glu Ile Asp Arg Lys Ile Leu Ala
 85 90 95
 Asp Ile Ala Val Phe Asp Lys Val Ala Phe Thr Ala Leu Val Glu Lys
 100 105 110
 Ala Lys Ala Ala Leu Ala
 115

<210> 395
 <211> 65
 <212> PRT
 <213> E. Coli

<400> 395
 Met Pro Lys Ile Lys Thr Val Arg Gly Ala Ala Lys Arg Phe Lys Lys
 1 5 10 15
 Thr Gly Lys Gly Gly Phe Lys His Lys His Ala Asn Leu Arg His Ile
 20 25 30

Leu Thr Lys Lys Ala Thr Lys Arg Lys Arg His Leu Arg Pro Lys Ala
 35 40 45
 Met Val Ser Lys Gly Asp Leu Gly Leu Val Ile Ala Cys Leu Pro Tyr
 50 55 60
 Ala
 65

<210> 396
 <211> 180
 <212> PRT
 <213> E. Coli

<400> 396
 Met Lys Gly Gly Lys Arg Val Gln Thr Ala Arg Pro Asn Arg Ile Asn
 1 5 10 15
 Gly Glu Ile Arg Ala Gln Glu Val Arg Leu Thr Gly Leu Glu Gly Glu
 20 25 30
 Gln Leu Gly Ile Val Ser Leu Arg Glu Ala Leu Glu Lys Ala Glu Glu
 35 40 45
 Ala Gly Val Asp Leu Val Glu Ile Ser Pro Asn Ala Glu Pro Pro Val
 50 55 60
 Cys Arg Ile Met Asp Tyr Gly Lys Phe Leu Tyr Glu Lys Ser Lys Ser
 65 70 75 80
 Ser Lys Glu Gln Lys Lys Gln Lys Val Ile Gln Val Lys Glu Ile
 85 90 95
 Lys Phe Arg Pro Gly Thr Asp Glu Gly Asp Tyr Gln Val Lys Leu Arg
 100 105 110
 Ser Leu Ile Arg Phe Leu Glu Glu Gly Asp Lys Ala Lys Ile Thr Leu
 115 120 125
 Arg Phe Arg Gly Arg Glu Met Ala His Gln Gln Ile Gly Met Glu Val
 130 135 140
 Leu Asn Arg Val Lys Asp Asp Leu Gln Glu Leu Ala Val Val Glu Ser
 145 150 155 160
 Phe Pro Thr Lys Ile Glu Gly Arg Gln Met Ile Met Val Leu Ala Pro
 165 170 175
 Lys Lys Lys Gln
 180

<210> 397
 <211> 642
 <212> PRT
 <213> E. Coli

<400> 397
 Met Pro Val Ile Thr Leu Pro Asp Gly Ser Gln Arg His Tyr Asp His
 1 5 10 15
 Ala Val Ser Pro Met Asp Val Ala Leu Asp Ile Gly Pro Gly Leu Ala
 20 25 30
 Lys Ala Cys Ile Ala Gly Arg Val Asn Gly Glu Leu Val Asp Ala Cys
 35 40 45
 Asp Leu Ile Glu Asn Asp Ala Gln Leu Ser Ile Ile Thr Ala Lys Asp
 50 55 60
 Glu Glu Gly Leu Glu Ile Ile Arg His Ser Cys Ala His Leu Leu Gly

65					70					75				80
His	Ala	Ile	Lys	Gln	Leu	Trp	Pro	His	Thr	Lys	Met	Ala	Ile	Gly
				85					90					95
Val	Ile	Asp	Asn	Gly	Phe	Tyr	Tyr	Asp	Val	Asp	Leu	Asp	Arg	Thr
			100					105					110	Leu
Thr	Gln	Glu	Asp	Val	Glu	Ala	Leu	Glu	Lys	Arg	Met	His	Glu	Leu
			115				120					125	Ala	
Glu	Lys	Asn	Tyr	Asp	Val	Ile	Lys	Lys	Lys	Val	Ser	Trp	His	Glu
			130			135					140		Ala	
Arg	Glu	Thr	Phe	Ala	Asn	Arg	Gly	Glu	Ser	Tyr	Lys	Val	Ser	Ile
145					150					155				160
Asp	Glu	Asn	Ile	Ala	His	Asp	Asp	Lys	Pro	Gly	Leu	Tyr	Phe	His
			165						170					175
Glu	Tyr	Val	Asp	Met	Cys	Arg	Gly	Pro	His	Val	Pro	Asn	Met	Arg
			180					185				190	Phe	
Cys	His	His	Phe	Lys	Leu	Met	Lys	Thr	Ala	Gly	Ala	Tyr	Trp	Arg
			195				200					205	Gly	
Asp	Ser	Asn	Asn	Lys	Met	Leu	Gln	Arg	Ile	Tyr	Gly	Thr	Ala	Trp
			210			215					220		Ala	Ala
Asp	Lys	Lys	Ala	Leu	Asn	Ala	Tyr	Leu	Gln	Arg	Leu	Glu	Glu	Ala
225					230					235				240
Lys	Arg	Asp	His	Arg	Lys	Ile	Gly	Lys	Gln	Leu	Asp	Leu	Tyr	His
			245						250					255
Gln	Glu	Glu	Ala	Pro	Gly	Met	Val	Phe	Trp	His	Asn	Asp	Gly	Trp
			260					265					270	Thr
Ile	Phe	Arg	Glu	Leu	Glu	Val	Phe	Val	Arg	Ser	Lys	Leu	Lys	Glu
			275				280					285		Tyr
Gln	Tyr	Gln	Glu	Val	Lys	Gly	Pro	Phe	Met	Met	Asp	Arg	Val	Leu
			290			295					300		Trp	
Glu	Lys	Thr	Gly	His	Trp	Asp	Asn	Tyr	Lys	Asp	Ala	Met	Phe	Thr
305					310					315				320
Ser	Ser	Glu	Asn	Arg	Glu	Tyr	Cys	Ile	Lys	Pro	Met	Asn	Cys	Pro
			325						330					335
His	Val	Gln	Ile	Phe	Asn	Gln	Gly	Leu	Lys	Ser	Tyr	Arg	Asp	Leu
			340					345					350	Pro
Leu	Arg	Met	Ala	Glu	Phe	Gly	Ser	Cys	His	Arg	Asn	Glu	Pro	Ser
			355				360					365	Gly	
Ser	Leu	His	Gly	Leu	Met	Arg	Val	Arg	Gly	Phe	Thr	Gln	Asp	Ala
					375						380			
His	Ile	Phe	Cys	Thr	Glu	Glu	Gln	Ile	Arg	Asp	Glu	Val	Asn	Gly
385					390					395				400
Ile	Arg	Leu	Val	Tyr	Asp	Met	Tyr	Ser	Thr	Phe	Gly	Phe	Glu	Lys
			405						410				415	Ile
Val	Val	Lys	Leu	Ser	Thr	Arg	Pro	Glu	Lys	Arg	Ile	Gly	Ser	Asp
			420					425					430	Glu
Met	Trp	Asp	Arg	Ala	Glu	Ala	Asp	Leu	Ala	Val	Ala	Leu	Glu	Glu
			435				440					445	Asn	
Asn	Ile	Pro	Phe	Glu	Tyr	Gln	Leu	Gly	Glu	Gly	Ala	Phe	Tyr	Gly
			450			455					460			Pro
Lys	Ile	Glu	Phe	Thr	Leu	Tyr	Asp	Cys	Leu	Asp	Arg	Ala	Trp	Gln
465					470					475				480
Gly	Thr	Val	Gln	Leu	Asp	Phe	Ser	Leu	Pro	Ser	Arg	Leu	Ser	Ala
			485						490				495	Ser
Tyr	Val	Gly	Glu	Asp	Asn	Glu	Arg	Lys	Val	Pro	Val	Met	Ile	His
			500					505				510	Arg	
Ala	Ile	Leu	Gly	Ser	Met	Glu	Arg	Phe	Ile	Gly	Ile	Leu	Thr	Glu
			515				520					525	Glu	Glu

Phe	Ala	Gly	Phe	Phe	Pro	Thr	Trp	Leu	Ala	Pro	Val	Gln	Val	Val	Ile
530						535					540				
Met	Asn	Ile	Thr	Asp	Ser	Gln	Ser	Glu	Tyr	Val	Asn	Glu	Leu	Thr	Gln
545					550					555					560
Lys	Leu	Ser	Asn	Ala	Gly	Ile	Arg	Val	Lys	Ala	Asp	Leu	Arg	Asn	Glu
			565						570					575	
Lys	Ile	Gly	Phe	Lys	Ile	Arg	Glu	His	Thr	Leu	Arg	Arg	Val	Pro	Tyr
			580					585					590		
Met	Leu	Val	Cys	Gly	Asp	Lys	Glu	Val	Glu	Ser	Gly	Lys	Val	Ala	Val
		595					600					605			
Arg	Thr	Arg	Arg	Gly	Lys	Asp	Leu	Gly	Ser	Met	Asp	Val	Asn	Glu	Val
	610					615					620				
Ile	Glu	Lys	Leu	Gln	Gln	Glu	Ile	Arg	Ser	Arg	Ser	Leu	Lys	Gln	Leu
625					630					635					640
Glu	Glu														

<210> 398
 <211> 450
 <212> PRT
 <213> E. Coli

<400> 398

Met	Thr	Lys	His	Tyr	Asp	Tyr	Ile	Ala	Ile	Gly	Gly	Gly	Ser	Gly	Gly
1			5						10					15	
Ile	Ala	Ser	Ile	Asn	Arg	Ala	Ala	Met	Tyr	Gly	Gln	Lys	Cys	Ala	Leu
			20					25					30		
Ile	Glu	Ala	Lys	Glu	Leu	Gly	Gly	Thr	Cys	Val	Asn	Val	Gly	Cys	Val
		35					40					45			
Pro	Lys	Lys	Val	Met	Trp	His	Ala	Ala	Gln	Ile	Arg	Glu	Ala	Ile	His
	50					55					60				
Met	Tyr	Gly	Pro	Asp	Tyr	Gly	Phe	Asp	Thr	Thr	Ile	Asn	Lys	Phe	Asn
65				70						75					80
Trp	Glu	Thr	Leu	Ile	Ala	Ser	Arg	Thr	Ala	Tyr	Ile	Asp	Arg	Ile	His
			85						90					95	
Thr	Ser	Tyr	Glu	Asn	Val	Leu	Gly	Lys	Asn	Asn	Val	Asp	Val	Ile	Lys
			100					105					110		
Gly	Phe	Ala	Arg	Phe	Val	Asp	Ala	Lys	Thr	Leu	Glu	Val	Asn	Gly	Glu
	115						120					125			
Thr	Ile	Thr	Ala	Asp	His	Ile	Leu	Ile	Ala	Thr	Gly	Gly	Arg	Pro	Ser
	130					135					140				
His	Pro	Asp	Ile	Pro	Gly	Val	Glu	Tyr	Gly	Ile	Asp	Ser	Asp	Gly	Phe
145					150					155					160
Phe	Ala	Leu	Pro	Ala	Leu	Pro	Glu	Arg	Val	Ala	Val	Val	Gly	Ala	Gly
			165						170					175	
Tyr	Ile	Ala	Val	Glu	Leu	Ala	Gly	Val	Ile	Asn	Gly	Leu	Gly	Ala	Lys
			180					185					190		
Thr	His	Leu	Phe	Val	Arg	Lys	His	Ala	Pro	Leu	Arg	Ser	Phe	Asp	Pro
	195						200					205			
Met	Ile	Ser	Glu	Thr	Leu	Val	Glu	Val	Met	Asn	Ala	Glu	Gly	Pro	Gln
	210					215					220				
Leu	His	Thr	Asn	Ala	Ile	Pro	Lys	Ala	Val	Val	Lys	Asn	Thr	Asp	Gly
225					230					235					240
Ser	Leu	Thr	Leu	Glu	Leu	Glu	Asp	Gly	Arg	Ser	Glu	Thr	Val	Asp	Cys
			245						250					255	
Leu	Ile	Trp	Ala	Ile	Gly	Arg	Glu	Pro	Ala	Asn	Asp	Asn	Ile	Asn	Leu

	260		265		270
Glu Ala	Ala Gly Val Lys Thr	Asn Glu Lys Gly Tyr Ile	Val Val Asp		
	275	280	285		
Lys Tyr	Gln Asn Thr Asn Ile	Glu Gly Ile Tyr Ala Val	Gly Asp Asn		
	290	295	300		
Thr Gly	Ala Val Glu Leu Thr Pro	Val Ala Val Ala Ala	Gly Arg Arg		
305	310	315	320		
Leu Ser	Glu Arg Leu Phe Asn Asn	Lys Pro Asp Glu His	Leu Asp Tyr		
	325	330	335		
Ser Asn	Ile Pro Thr Val Val Phe	Ser His Pro Pro Ile	Gly Thr Val		
	340	345	350		
Gly Leu	Thr Glu Pro Gln Ala Arg	Glu Gln Tyr Gly Asp	Asp Gln Val		
	355	360	365		
Lys Val	Tyr Lys Ser Ser Phe Thr	Ala Met Tyr Thr Ala	Val Thr Thr		
	370	375	380		
His Arg	Gln Pro Cys Arg Met Lys	Leu Val Cys Val Gly	Ser Glu Glu		
385	390	395	400		
Lys Ile	Val Gly Ile His Gly Ile	Gly Phe Gly Met Asp	Glu Met Leu		
	405	410	415		
Gln Gly	Phe Ala Val Ala Leu Lys	Met Gly Ala Thr Lys	Lys Asp Phe		
	420	425	430		
Asp Asn	Thr Val Ala Ile His Pro	Thr Ala Ala Glu Glu	Phe Val Thr		
	435	440	445		
Met Arg					
450					

<210> 399
 <211> 2904
 <212> RNA
 <213> E. Coli

<400> 399

aagguuaagc	cucacgguuc	auuaguaccg	guuagcucaa	cgcaucgcug	cgcuuacaca	60
cccggccuau	caacgucguc	gucuucaacg	uuccuucagg	acccuuaaag	ggucagggag	120
aacucaucuc	ggggcaaguu	ucgugcuuag	augcuuucag	cacuuauauc	uuccgcuuuu	180
agcuaccggg	cagugccaau	ggcaugacaa	cccgaacacc	agugaugcgu	ccacuccggu	240
ccucucguac	uaggagcagc	ccccucagu	ucuccagcgc	ccacggcaga	uagggaccga	300
acugucucac	gacguucuaa	acccagcucg	cguaccacuu	uaaauaggcg	acagccauac	360
ccuuggggacc	uacuucagcc	ccaggauug	augagccgac	aucgaggugc	caaacaccgc	420
cgucgauaug	aacucuuggg	cgguaucagc	cuguuaucac	cggaguaccu	uuuauccguu	480
gagcgauggc	ccuuccauuc	agaaccaccg	gaucacuaug	accugcuuuc	gcaccugcuc	540
gcgcgcgucac	gcucgcaguc	aagcuggcuu	augccauugc	acuaaccucc	ugauguccga	600
ccaggauuag	ccaaccuucg	ugcuccuccg	uuacucuuaa	ggaggagacc	gccccaguca	660
aacuacccac	cagacacugu	ccgcaaccgg	gauuacgggu	caacguuaga	acaucaaaca	720
uuaaaggggug	guauuucaag	gucggcucca	ugcagacugg	cguccacacu	ucaaagccuc	780
ccaccuaucc	uacacaucaa	ggcucaaugu	ucagugucaa	gcuauaguaa	agguuacagg	840
ggucuuuuccg	ucuugccgcg	gguacacugc	aucuucacag	cgaguucaau	uucacugagu	900
cucggggugga	gacagccugg	ccaucauuac	gccauucgug	caggucggaa	cuuacccgac	960
aaggaaauuuc	gcuaccuuag	gaccguuaua	guuacggccg	ccguuuaccg	gggcuucgau	1020
caagagcuuc	gcuugcgcua	accccaucaa	uuuaccuucc	ggcaccgggc	aggcgucaca	1080
ccguauacgu	ccacuucgu	guuugcacag	ugcuguguuu	uuauuaaaca	guugcagcca	1140
gcugguauc	ucgacugauu	ucagcuccau	ccgcgaggga	ccucaccuac	auaucagcgu	1200
gccuucuccc	gaaguuacgg	caccuuuuug	ccuaguuccu	ucacccgagu	ucucucaagc	1260
gccuugguau	ucucuaccug	accaccugug	ucgguuuggg	guacgauuug	auguuaccug	1320
augcuuagag	gcuuuuccug	gaagcagggc	auuuguugcu	ucagcaccgu	agugccucgu	1380

caucacgccu	cagccuugau	uuuccggauu	ugccuggaaa	accagccuac	acgcuuaaac	1440
cgggacaacc	gucgcccggc	caacauagcc	uucuccgucc	cccuuucgca	guaacaccaa	1500
guacaggaau	auuaaccugu	uucccaucga	cuacgccuuu	cggccucgcc	uuaggggucg	1560
acucacccug	ccccgauuaa	cguuggacag	gaacccuugg	ucuuccggcg	agcgggcuuu	1620
ucacccgcuu	uauuguuacu	uauugucagca	uucgcacuuu	ugauaccucc	agcaugccuc	1680
acagcacacc	uucgcaggcu	uacagaacgc	uccccuaccc	aacaacgcau	aagcgucgcu	1740
gccgcagcuu	cggugcaugg	uuuagccccg	uuacauuuu	cgcgcaggcc	gacucgacca	1800
gugagcuauu	acgcuuucuu	uaaauauggg	cugcuucuaa	gccaacaucc	uggcugucug	1860
ggccuuccca	caucguuucc	cacuaaacca	ugacuuuggg	accuuagcug	gcggucuggg	1920
uuguuucccu	cuucacgacg	gacguuagca	cccgcggugu	gucucccgug	auaacaauuc	1980
ccgguaauucg	caguugcau	cggguuggua	agucgggaug	acccccuugc	cgaaacagug	2040
cucuaccccc	ggagaugaau	ucacgaggcg	cuaccuaaa	agcuuucggg	gagaaccagc	2100
uauccccggg	uuugauuggc	cuuucacccc	cagccacaag	ucauccgcua	auuuuucaac	2160
auuagucggg	ucgguccucc	aguauuguu	acccaaccuu	caaccugccc	auggcuaugu	2220
caccggguuu	cgggucuaau	cccugcaacu	uaacgcccag	uuaagacucg	guuucccuuc	2280
ggcuccccua	uucgguaaac	cuugcuacag	aaauaaaguc	gcugacccau	uauacaaaag	2340
guacgcaguc	acacgccuaa	gcgugcuccc	acugcuugua	cguacacggu	uucagguucu	2400
uuuucacucc	ccucgcgggg	guucuuuucg	ccuuucccuc	acgguacugg	uucacuaucg	2460
gucagucagg	aguauuuagc	cuuggaggau	ggucccccc	uauucagaca	ggauaccacg	2520
ugucccgccc	uacucaucga	gcucacagca	ugugcauuuu	uguguaacgg	gcugucaccc	2580
uguaucgcgc	gccuuuccag	acgcuuuccc	uaacacacac	acugauucag	gcucugggcu	2640
gcuccccguu	cgcucgcggc	uacuggggga	aucucggguu	auuucuuuuu	cucggggguac	2700
uuagauguuu	caguuccccc	ggucgcccuc	auuaaccuau	ggauucaguu	aaugauagug	2760
ugucgaaaca	cacugggguu	ccccauucgg	aaucgcccgg	uuauaacggu	ucauauaccc	2820
uuaccgacgc	uuaucgcaga	uuagcacguc	cuucaucgcc	ucugacugcc	agggcaucca	2880
ccguguacgc	uuagucgcuu	aacc				2904

<210> 400
 <211> 120
 <212> RNA
 <213> E. Coli

<400> 400

augccuggca	guucccuacu	cucgcauggg	gagacccac	acuaccaucg	gcgcuaacggc	60
guuucacuuc	ugaguucggc	auggggucag	gugggaccac	cgcgcuaacgg	ccgccaggca	120

<210> 401
 <211> 76
 <212> RNA
 <213> E. Coli

<400> 401

gucccccucg	ucuagaggcc	caggacaccg	cccuuucacg	gcgguaacag	ggguucgaau	60
ccccuagggg	acgcc					76

<210> 402
 <211> 1549
 <212> RNA
 <213> E. Coli

<400> 402

<400> 405
caggtggtat ggaaacccaa aatggagacg ggaagctgaa ccagatagtt actggaggtg 60
atcaccagca gatgaaataa cgataaccag aacaacgcct tatagcgttg agtttgcgag 120
aaaacgttca tattgtacct ttttgattaa ccattgggg 159

<210> 406
<211> 640
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(640)
<223> n = A,T,C or G

<400> 406
ggggnccaaa gtgtttgggn cgggcaactg gaggccaacc ttaanttnng ggaaatTTTT 60
aanaaaaggc ggggatttgt nagccacggg ngattanttt anaataaatt aagtgttgcc 120
ataaggggac aaagngaagg aagtggntat taanggannc gccaatgcga nttagggcag 180
accattcggc cattcgccctt cttggttatc gaagttcatc cagatagccg ttgccngacc 240
gaccagattc gcttcnggca caaagcccca gtaacggctg tccgcgctgt tgcgcgggtt 300
gtogcccatc atgaagtatt gtcccggagg aacaatccag gttgccagtt gttgccctgg 360
ctgctggtaa tacatcccca cctgatcctg cgcaatcggc actgtcagaa tgcgggtgcgt 420
cacatcccc agtgtctctt tacgctcgga aagacgaatt ccattttctt tggtttcggt 480
tttcggcaact tcaaagaatc cgctggtcgc ttccccacca ttacggcgtg agaaggtctg 540
aacgaaatcg ctcggttcca cgtttgagta ggtgaccggc agcgcgtttt cacacgcctg 600
gccggaactg catcccgggt gaatcgtcag ctcttttgag 640

<210> 407
<211> 682
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(682)
<223> n = A,T,C or G

<400> 407
cctgcagggt aatgtcgcca ttaaactggc gcaggcagcc aaagagttgc tccgcttcta 60
cccagtcggc agcgacaact tgcgttaaag tcgcaaaatt atcatctgca ctcaactgcgt 120
gacgtaagcg gatggagtg cgggaaacct catagtgacc gccaccaggt tggcctgcat 180
cgctttgtag cgtacgcgcg gcattggcaa taagattcag ataactcagac tcttccgggg 240
ccttcgccag cataaaagag gaggatgctc gcgtatgcag caactgctcc agcgcaaatt 300
gcagccgchg ttgagtatca ctgaataaag gatcgtttgc gtcaatcaaa tgtggctgag 360
caaataattc ctgatagcta tcggtatcag gaaccaggtc acgccatgca agtttcgtaa 420
tgggtcaaagt tgatgttttt tagtctgttg tcaaagccgc nattataccn gtaaccggca 480
ctacagcaca cgtagaaagc accgcacaat actcctggca tgggcgttaa agctcacagg 540
atggagatct tttcttcaact ggcctaaaaa gctgatattc tgtaaaagagt tacacngtaa 600
cattgagatc gctatgaaat atcaacaact tggaaaatct tgnaaagcng gttggaaaat 660
ggaaagtatc tgggttaagaa gc 682

<210> 408
<211> 309
<212> DNA
<213> Escherichia coli

<400> 408
 ggggatccgg cagaatttta cgctgaccaa tgacgcgacg acgtggcatg gaaatactcc 60
 gttgttaatt caggattgtc caaaactcta cgagtttagt ttgacattta agttaaaacg 120
 tttggcctta cttaacggag aaccattaag ccttaggacg cttcacgcca tacttggaac 180
 gagcctgctt acggtcttta acgccggagc agtcaagcgc accacgtacg gtgtggtaac 240
 gaacaccogg gaggtcttta acacgaccgc cacggatcag gatcacggag tgctcctgca 300
 gccaaagctt 309

<210> 409
 <211> 1167
 <212> DNA
 <213> Escherichia coli

<400> 409
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 tggaacactt tccgcaatgc ctggtgctat cacgcttaaa ccatttcatt gcgatttaca 120
 cagaacggac gtccctgtcg agtatattaa gtgcgtcgata gaaacaagca ttgaaaggca 180
 cagcagtagt caaacagtgt gaaacgctac tggcgcccta cagcgcaaaa aggctggtga 240
 ctaaaaagtc accagccatc agcctgattt ctcaggctgc aaccggaagg gttggcttat 300
 ttaacttcaa cttcagcgcc agcttcttcc agagcttttt tcagtgtctc tgcgtcgtct 360
 ttgctcacgc cttctttcag agcagccggg gcagattcta ccaggtcttt agcttctttc 420
 agaccaggc cagttgcgcc acgtactgct ttgataacag caactttggt agcgccagca 480
 gctttcagaa ttacgtcgaa ttcagttttt tcttcagcag cttcaaccgg gccagcagct 540
 acagctacag cagcagcagc ggaaacaccg aatttttctt ycattgcaga gatcaagttc 600
 tacaacgtcc attacagaca tagctgcaac tgcttcaatg awttgatctt tagtgataga 660
 catttaaatk gttcctgaat atcagaataa gtttatacgt aagcgaatgc gttaaaaaga 720
 taactgcgaw taagcagctt ytttcgcac gcgtacagma gccagagtac gaaccagttt 780
 gccagccgaa gcttctttca tggttgccat caggcgtgca attgcttctt cgtaggctcg 840
 cagagttgcc aggcgggtcg tctgagacgc cgggatcagc tcaccttcaa aggcagcggc 900
 tttgacctca aattttgcat tcgctttcgc gaactctttg aacagacgag cagcagcggc 960
 cgggtgttcc atagagtatg caatcagggt cggaccaaca aacgcgtctt tcaggcactc 1020
 gaacggagta ctttcaacag cacggcgcag cagggtgtta cgaacaacac gcatgtatac 1080
 gccagcttcg cgacctgctt tacgcagttc agtcatttta totacagtta cgcccacggg 1140
 aatccgcaac tactgcaagc caagctt 1167

<210> 410
 <211> 404
 <212> DNA
 <213> Escherichia coli

<400> 410
 caacmctatt ttgktggacc ggaaaakgga acactttccg cawkgcctgt tgctatcacg 60
 cttaaaccat ttcatgcgga tttacacaga acggacgtcc tgtcgcagta tattaagtcg 120
 tcgatagaaa caagcattga aaggcacagc agtagtcaaa cagtgtgaaa cgctactggc 180
 gccttacagc gcaaaaaggc tgggtgactaa aaagtcacca gccatcagcc tgattttctca 240
 ggctgcaacc ggaagggttg gcttatttaa cttcaacttc agcgccagct tcttccagag 300
 cttttttcag tgcttctgcg tcgtctttgc tcacgccttc tttcagagca gccgggtgcag 360
 attctaccag gtcttttagct tctttcagac ccaggccagt tgcg 404

<210> 411
 <211> 152
 <212> DNA
 <213> Escherichia coli

<400> 411
 agagcttttt tcagtgtctc tgcgtcgtct ttgctcacgc cttctttcaa gagcagcccg 60
 gtgcagattc taccaggtct ttagcttctt tcagaccag gccagttgcg ccacgtactg 120

ctttgataac agcaactttg ttagcgccag ca

152

<210> 412

<211> 825

<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<222> (1)...(825)

<223> n = A,T,C or G

<400> 412

gatccgtoga	cccatctgtc	cattgagcgg	acagtttgtg	caacactatt	ttgttgaccg	60
gaaaatggaa	cactttccgc	aatgcctggt	gctatcacgc	ttaamccatt	tcattgcgat	120
ttacacagaa	cggacgtcct	gtcgcagtat	attaagtcgt	cgatagaaac	aagcattgaa	180
aggcacagca	gtagtcaaac	agtgtgaaac	gctactggcg	ccttacagcg	caaaaaggct	240
ggtgactaaa	aagtcaccag	ccatcagcct	gatttctcag	gctgcaaccg	gaagggttgg	300
cttattttaac	ttcaacttca	gcgccagcct	cttcagagc	ttttttcagt	gcttctgcgt	360
cgtcttttgt	cacgccttct	ttcagagcag	ccgggtgcag	attctaccag	gtcttttagct	420
tctttcagac	ccaggccagt	tgcgccacgt	actgctttga	taacagcaac	tttgtttagcg	480
ccagcagctt	tcagaattac	gtcgaattca	agttttttct	tcagcagctt	caaccgggcc	540
agcagctaca	gtacacagcag	cagcagcggg	aacaccgaat	ttttcttyca	ttggcagaga	600
tcaagttcta	caacgtccat	tacagacata	gctgcaactg	cttcaatgat	tkgatcttwa	660
gtgatagaca	tttaaattgt	tcctgaatat	cagaataagt	ttatacgtaa	gcgaatgcgt	720
taaaaagata	actgcgatta	agcagcttct	ttcgcatcgc	gtacagcagc	cagaggtcga	780
accagtttgc	cagccgaagg	ttggcttttc	agcctnnnnc	natta		825

<210> 413

<211> 425

<212> DNA

<213> Escherichia coli

<400> 413

agtagtcaaa	caggtgkgra	acgctactgg	cgccttacag	cgcaaaaagg	ctggtgacta	60
aaaagtcacc	agccatcarc	ctgattttct	aggctgcaac	ccggaagggt	tggtttatct	120
aacttcaact	tcagcgccag	cttcttccag	agcttttttc	agtgttcttg	cgtcgtcttt	180
gtcacgcct	tctttcagag	cagccgggtg	agattctacc	aggcttttag	cttctttcag	240
accaggcca	gttgcgccac	gtactgcttt	gataacagca	actttgttag	cgccagcagc	300
tttcagaatt	acgtcgaatt	cagttttttc	ttcagcagct	tcaaccgggc	cagcagctac	360
agctacagca	gcagcagcgg	aaacaccgga	atttttcttc	cattgcagag	atcaagttct	420
acaac						425

<210> 414

<211> 126

<212> DNA

<213> Escherichia coli

<400> 414

agagcttttt	tcagtgtctc	tgcgtcgtct	ttgctcacgc	cttctttcag	agcagccggt	60
gcagattcta	ccagggtctt	agcttctttc	agaccagggc	cagttgcgcc	acgtactgct	120
ttrata						126

<210> 415

<211> 264

<212> DNA

<213> Escherichia coli

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<400> 415
ctgcmaccog garggggttg otaattttaac ttcaacttca gcgccagctt cttycagagc 60
ttttttcaag tgctttctgcg tegtctttgc tcacgccttc tttcagagca gccgggtgcag 120
attctaccag gtcttttagct tctttcagac ccaggccagt tgcgccacgt actgctttga 180
taacagcaac tttgttagcg ccagcagctt tcagaattac gtcgaattca gttttttctt 240
cagcagcttc aaccgggcca gcag 264

<210> 416
<211> 201
<212> DNA
<213> Escherichia coli

<400> 416
cgcataccct gcagcatcgg ccgatggag atcaggctcg cagaacgctg taccgctttg 60
taggtggtgt taccggtgtt cagatccggg aagatgaaca cggtagcgcg acctgcaacc 120
ggagagtctg gcgctttgga tttcgcaacg tcagccatta ccgcagcgtc gtactgcagc 180
ggaccgtcga tcatcaggtc a 201

<210> 417
<211> 239
<212> DNA
<213> Escherichia coli

<400> 417
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gcttttttta ttattccgtg acttccagcg tagtgaaggc aaacttctcg ccatcaaata 120
gccctgact ggtaggtttt agcgcgggga tcaactggcg agaaagaaac gccatctgaa 180
taaacggctc atcgggtaac ggaccgcatt cacgggcggc ggctttcaag gcgtcaatt 239

<210> 418
<211> 223
<212> DNA
<213> Escherichia coli

<400> 418
ttcttttttt cgtcaacggt gtccagaatc atttttattta cctcgggtac ttatgctgat 60
ttttattatt atggggaagg tggtatttat gagtttcatt tatgccgtaa cgacaatgaa 120
ctcgggaatt agtataagca gcgcgagaat aataatcatt gtgcaaatgc taatttaatt 180
aatactatctt aaatattatt ttgagcatat gcacataagg ttg 223

<210> 419
<211> 223
<212> DNA
<213> Escherichia coli

<400> 419
ttcttttttt cgtcaacggt gtccagaatc atttttattta cctcgggtac ttatgctgat 60
ttttattatt atggggaagg tggtatttat gagtttcatt tatgccgtaa cgacaatgaa 120
ctcgggaatt agtataagca gcgcgagaat aataatcatt gtgcaaatgc taatttaatt 180
aatactatctt aaatattatt ttgagcatat gcacataagg ttg 223

<210> 420
<211> 212
<212> DNA
<213> Escherichia coli

<400> 420
aatagcgggt atgcacgcct ttcttttttt cgtcaacggt gtccagaatc atttttattta 60
cctcgggtac ttatgctgat ttttattatt atggggaagg tgttatttat gagtttcatt 120
tatgccgtaa cgmcaatgaa ctccggaatt agtataagca gcgcgagaat aataatcatt 180
gtgcaaattgc taattttaatt aatactattt aa 212

<210> 421
<211> 438
<212> DNA
<213> Escherichia coli

<400> 421
ccctgtaaat tatcgcccggt ggcataaaaa ctgcggtccaa acgccgtctt tgccagcagc 60
caggccataa atgccaccag aattatcgtc aaccaaccaa ttgctgaaac gccaaagcagc 120
agcggggcgg agagctgttt cagttcggcg ggtaaccctt caatccattt gccgccagtc 180
cacagcaaca tgatgcctct gtacaaccct aacgtgccaa ggggtggcaac aatggcaggg 240
atcttttagcc acgcgaccag gacaccgttg aaaaatcccg cgagcaaacc aagcagtaaa 300
gtcgcgacac aagcaacagg tagtgaatat cctgcgttca gtaacatccc caacagcacc 360
gogcacattc cgggtaatcg aaccccactt gaaacatcaa tattgsgsgt aagcattwcc 420
aagcgttcgs gcccatkg 438

<210> 422
<211> 682
<212> DNA
<213> Escherichia coli

<400> 422
aattcccggt gatccgtoga ccgtgcgctt ccggttgtgg caaccgcgga aatggcgcg 60
cggttaagtat ggcgggggta ttcttccccc gttgaggaca ccgggttgct aggttgacca 120
tacgcttaag tgacaacccc gctgcaacgc cctctgttat caattttctg gtgacgtttg 180
gcggtatcag ttttactcog tgactgctct gccgcccttt ttaaagtga ttttgtgatg 240
tggtgaatgc ggctgagcgc acgcggaaca gttaaaacca aaaacagtgt tatgggtgga 300
ttctctgtat ccggcggttaa ttgttaactg gttaacgtca cctggaggca ccaggcactg 360
catcacaaaa ttcatgtgtg aggaacgcgat aatgaaaacg ttattaccaa acgttaatac 420
gtctgaaggt tgttttgaaa ttggtgtcac tatcagtaac ccagtattta ctgaagatgc 480
cattaacaag agaaaacaag aacgggagct attaaataaa atatgcattg tttcaatgct 540
ggctcgttta cgtctgatgc caaaaggatg tgcacaatga attcagcatt tgtgcttggt 600
ctgacagttt ttcttggttc cggagagcca gttgatattg cagtcagtgt tcacaggaca 660
atgcaggagt gatgactgca gc 682

<210> 423
<211> 600
<212> DNA
<213> Escherichia coli

<400> 423
ggggatccga ttgtgactgc tctgcgcgcc tttttaaagt gaattttgtg atgtggtgaa 60
tgcggtcgag cgcacgcgga acagttaaaa ccaaaaacag tgttatgggt ggattctctg 120
tatccggcgt taattgttaa ctgggttaacg tcacctggag gcaccaggca ctgcatcaca 180
aaattcattg ttgaggacgc gataatgaaa acgttattac caaacgttaa tacgtctgaa 240
ggttggtttg aaattggtgt cactatcagt aaccacgtat ttactgaaga tgccattaac 300
aagagaaaaa aagaacggga gctattaaat aaaatatgca ttgtttcaat gctggctcgt 360
ttacgtctga tgccaaaagg atgtgcacaa tgaattcagc atttgtgctt gttctgacag 420
tttttcttgt ttccggagag ccagttgata ttgcagtcag tggtcacagg acaatgcagg 480
agtgtatgac tgcagcaacc gaacagaaaa ttcccggtaa ctgttaccgc gtcgataaag 540
ttattcacca ggataatatc gaaatcccgg caggtcttta aacagttccg taataaataa 600

<210> 424
 <211> 100
 <212> DNA
 <213> Escherichia coli

<400> 424
 gggatccagc aagaagatgc ggttgtaccg tcatcacgca gatgcgcaaa gctactcagc 60
 aactgacctt tcttcgcaat aagcacgcca ttagcgctcat 100

<210> 425
 <211> 465
 <212> DNA
 <213> Escherichia coli

<400> 425
 tcgogtgttt accttcaaca tcggtaactt tctggcggat agtttcacgg taagcaacct 60
 gcggtttacc tacgttcgct tcaacgttga attcacgctt catacggcca acgatgatgt 120
 cgaggtgcag ttccgccata cccgcgatga tggctctggt agattcttcg tcagtccata 180
 cacggaaaga cgggtcttct ttagccagac ggcccagagc cagaccatt ttttcctggt 240
 cagcttttgt tttcggttca actgcgatgg agattaccgg ctccagggaat tccatacgtt 300
 ccagaatgat cggcgcaccc gggtcacaca ggggtgtcacc agtgggttac tctttcagac 360
 cgatagcagc agcgatgtcg cccgcgcgaa cttctttgat ctcttcacgt ttgttagcgt 420
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<210> 426
 <211> 653
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(653)
 <223> n = A,T,C or G

<400> 426
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 cagccagttt aaacgccagt tcagaggagt caacgtcatg gtaagaaccg aagtgcagac 120
 gaatacccat gtctactacc gggtagcctg ccagcggacc tgctttcagc tgttcctgga 180
 tacctttatc aacggccggg atgtattcgc cagggattac accaccttta atgtcgttga 240
 tgaactcgta gcctttcggg tttgaaccgg gctccagcgg gtacatgtcg ataacaacat 300
 gaccatactg accaogacca ccagactgtt tcgcgtgttt accttcaaca tcggtaactt 360
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 ggctgggtag attcttcgct agtccataca cggnaagacg ggtcttnttt agccagacgg 540
 gccagagnca gacccatttt tttctggcag ctttggnttc ggtcaactgc gatggaaata 600
 cccggctcaa ggaattcata cgtttcanaa tgatcggggc attccgggtc aca 653

<210> 427
 <211> 268
 <212> DNA
 <213> Escherichia coli

<400> 427
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 agtcaacgtc atggtaagaa ccgaagtgc gacgaatacc catgtctact accgggtagc 120
 ctgccagcgg acctgctttc agctgttcct ggataccttt atcaacggcc gggatgtatt 180
 cgccagggat tacaccacct ttaatgtcgt tgatgaactc gtagcctttc gggtttgaac 240

ccggctccag cgggtacatg tcgataac

268

<210> 428

<211> 330

<212> DNA

<213> Escherichia coli

<400> 428

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atgactgatt	gccgatacct	gattaaacgg	gtcatcaaaa	tcattcattgc	tgttttacag	120
ctgatccttc	tggtctttata	acacaaggaa	acgtacttaa	ggtgcgtccg	gtgaaccagt	180
cggacgcacc	tttaataact	ataaataagt	gtctgggcag	atactatata	aattaactta	240
gtgaatgatt	atgctaattg	catcaattaa	ataaatataa	tggcgtaaag	gcttcccagt	300
aataataatta	atactctact	tccagagtag				330

<210> 429

<211> 465

<212> DNA

<213> Escherichia coli

<400> 429

gttttgaggga	gatgtaagg	ctaattctgaa	tggctgcatt	ccttgtttaa	ggaaaaacga	60
atgactgatt	gccgatacct	gattaaacgg	gtcatcaaaa	tcattcattgc	tgttttacag	120
ctgatccttc	tggtctttata	acacaaggaa	acgtacttaa	ggtgcgtccg	gtgaaccagt	180
cggacgcacc	tttaataact	ataaataagt	gtctgggcag	atactatata	aattaactta	240
gtgaatgatt	atgctaattg	catcaattaa	ataaatataa	tggcgtaaag	gcttcccagt	300
aataataatta	atactctact	tccagagtag	aatattaaat	tttatccgcg	tggtgcatca	360
gcacaaattt	atcccacaac	tggtcttctg	tctcgacatg	cgccggatct	ttcacaatag	420
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<210> 430

<211> 379

<212> DNA

<213> Escherichia coli

<400> 430

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acaaggaaac	gtacttaagg	tgcgtccggg	gaaccagtcg	gacgcacctt	taataactat	180
aaataagtgt	ctgggcagat	actatataaa	ttaacttagt	gaatgattat	gctaattgtca	240
tcaattaaat	aaatataatg	gcggttaaggc	ttcccagtaa	tataattaat	actctacttc	300
cagagtagaa	tattaaattt	tatccgcgtg	gtgcatcagc	acaaatttat	cccacaactg	360
ttctttctgtc	tcgacatgc					379

<210> 431

<211> 443

<212> DNA

<213> Escherichia coli

<400> 431

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attagtttat	ttcaaagtag	gaaaatctcc	cggcgaaaaa	accgggagat	gaaagtgtga	180
tgggtatcaa	ataaacaaca	gaggagaaat	ttttaacgca	gccattcagg	caaatcgttt	240
aatcccattg	cctggcggat	aagttgcggc	ttaacgccag	gaagcgtgtc	ggccagtttc	300
aaaccaatat	cacgcagcag	ttttttcgcc	ggattgggtac	cggaaaacag	atcgcggaat	360
ccctgcatac	cagccagcat	caacgcgcga	ctgtgcttgc	ggctacgctc	atagcgacgc	420

agataaatgt actgcccgat gtc

443

<210> 432

<211> 638

<212> DNA

<213> Escherichia coli

<400> 432

caggggggttt	gttgtgggca	atgatgcatt	taagttatcg	tctgcagata	gaggagatat	60
tacaataaac	aacgaatcag	ggcatttgat	agtcaatacc	gcaattctat	caggagatat	120
agtcactcta	agaggaggag	aaattagggt	ggtattatag	cttgtgcgcg	ccatgattgg	180
cgcgcaatth	aaacttagtg	ctttacatcg	ctattgtctt	gatttccttg	aattatttta	240
taaattaaaa	aaacgactgt	tatgtataag	caaaggtccg	aacgaaaaat	acattccaaa	300
taaatgcttg	cttaaatctc	tatatccttc	cccgaaaaat	gacacataaa	attgagatat	360
tccaaaaaga	gatactacaa	ataaagatgc	ctttatttta	ttatttctaa	taaaaaataga	420
agcaataaaa	aataataaca	atgatataaa	tctaattgtt	ttaaatatat	tgtcttttat	480
gtttagtaata	gtcgttagta	tgtttgattc	tccatatatt	acgtgtagtt	ttttatatac	540
atggaaataa	ttttctttat	actgagacat	cacaccatca	tcaaattggaa	gtttgaagat	600
ggtgcttggt	ttgctaacca	ataaaaagag	tgcattcg			638

<210> 433

<211> 299

<212> DNA

<213> Escherichia coli

<400> 433

ctttacctgg	catgatccac	ttcgccagaa	taccggcaat	aagcccaaaa	ataatccatg	60
acagaatgcc	cattgtttcc	tcacttatct	gttttgacatt	agcgggttag	tcgctgataa	120
aaagcatagg	acaacatcgg	gagggcaaga	tttgtgacga	gcatcacgga	ggtttttttg	180
cgatggcgca	gaaattgcgc	catcaacgat	cagtgataat	taccaaccac	aaacatcatg	240
ttcgttttcc	gtgtcataag	aacgtacggt	attcaccaga	tcttttatca	cttcagccg	299

<210> 434

<211> 388

<212> DNA

<213> Escherichia coli

<400> 434

gaaaaaggag	gcaatatcgg	gtaaaggcat	tagcccgacg	aatacgtcgg	gctacaaaata	60
ttattgtgct	gcagggtgtt	tagcgggttg	ttgatccaca	ggttctaact	ggaagaccac	120
atcgacctga	tcatcaaaact	gaatagcggc	ctgctcgtaa	gtttcctggg	cggacaccgg	180
cgcggcacat	gctttcatca	tcgcacccat	tgggctgggc	tgatagttag	aaacatggta	240
gcgcacgcta	tataccggcc	ccagttttac	atgaaagccg	ttcgccagtt	cctgcgcctg	300
atgaatcgcg	ttatcaatcg	ctgcctttac	cgctttgtct	ttataggcat	ccggctgcgc	360
cacgcccagc	gacacagaac	gaattccc				388

<210> 435

<211> 351

<212> DNA

<213> Escherichia coli

<400> 435

ctatccttga	tgaaccgcgc	agcaaagata	ggtgattacg	tcatggtttt	acagaaaatt	60
acagaaaaag	gaggcaatat	cgggtaaagg	cattagcccgc	acgaatacgt	cgggctacaa	120
atattattgt	gctgcagggt	ttttagcggg	ttgttgatcc	acaggttcta	actggaagac	180
cacatcgacc	tgatcatcaa	actgaatagc	ggcctgctcg	taagtttcct	ggcgcgacac	240
cggcgcgcca	tcggctttca	tcatccgcac	cattgggctg	ggctgatagt	tggaaacatg	300

gtagcgcacg ctatataccg gccccagttt acgatgaaag ccgttcgccca g 351

<210> 436
<211> 762
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(762)
<223> n = A,T,C or G

<400> 436
aattatgaaa cactgtctgg aatcgtctga atgacgggca catttgcgag cacgcatcca 60
gtaataacac aggaaactat tttatctacg cgttagcgat agactgcttg catggcgaaa 120
ggaggttaagc cgacgatttc agcgggacgc tgaaacggga aagcccctcc cgaggaaggg 180
gccataaata aggaaagggg catgatgaag ctactcatca tcgtgggtgct cttagtcata 240
agcttccccg cttactaaga ctaccagggc gggggaaacc ccgctctacc ctactcctg 300
aaagtatgcc ttacagataa gattgtcaat ccgcaggctt tgtagtctgc gatcctgccca 360
gcaaatatte tttgcgagtc gttacgcaat aatcacagag gaaactattt tattcacgcg 420
ttagcgatag actgcattca gggcgaaagg aggtaagccg atgatttcag cgggacgctg 480
aaacgggaaa gcctctcccg gagaagaggg cttttaataa ggaaaggggt atgatgaagc 540
acgtcatcat actggtgata ctcttagtga ttagcttcca ggcttactaa gaacaccagg 600
gggaggggga aacctotttc taacctcac ttctgaaatt gggtgctatg acgctggcgt 660
tactgcttan cgctaccagt ttgtctgccc tggcggtgtg aacgccagat cggtagccgt 720
ttggatattt taatgaaagc cgacaaatca atcancgtga cg 762

<210> 437
<211> 292
<212> DNA
<213> Escherichia coli

<400> 437
cacatttgcg agcacgcac cagtaataac acaggaaact attttatcta cgcgttagcg 60
atagactgct tgcattggcg aaggaggtta gccgacgatt tcagcgggac gctgaaacgg 120
gaaagcccct cccgaggaag gggccataaa taaggaaagg gtcattgatga agctactcat 180
catcgtggtg ctcttagtca taagcttccc cgcttactaa gactaccagg gcgggggaaa 240
ccccgctcta ccctcactcc tgaaagtatg ctttcacgat aagattgtca at 292

<210> 438
<211> 631
<212> DNA
<213> Escherichia coli

<400> 438
atttacactt tttacgaaat catgggatca ctaacaaaat atcgcttgtc agttatattg 60
tatggcagga aagatatgag actgatatta cagatcccca aagtggagag tttatgacca 120
ttaaaaaataa gatgttgctg ggtgcgcttt tgctggttac cagtgcgccc tgggcccgcac 180
cagccaccgc gggttcgacc aatacctcgg gaatttctaa gtatgagtta agtagtttca 240
ttgctgactt taagcatttc aaaccagggg acaccgtacc agaaatgtac cgtaccgatg 300
agtacaacat taagcagtgg cagttgcgta acctgcccgc gcctgatgcc gggacgcact 360
ggacctatat gggtggcgag tacgtgttga tcagcgacac cgacggtaaa atcattaaag 420
cctacgacgg tgagattttt tatcatcgct aaaaaagcc ccctcatcat gagggggaaa 480
tgacagacac ttgttatttt ttattattag ccacttgctc gtcttgcttg ttattagtcg 540
tatttcacgt tgattaatgc ggttgccctc agtgcgccag atttaacttt gtttgatcgc 600
tagacgtagt aactggctgt tatcggaatt g 631

<210> 439
 <211> 566
 <212> DNA
 <213> Escherichia coli

<400> 439
 tatggcagga aagatatgcg actgatatta cagatcccca aagtggagag tttatgacca 60
 ttaaaaataa gatgttgctg ggtgcgcttt tgctgggttac cagtgccgcc tgggccgcac 120
 cagccaccgc gggttcgacc aatacctcgg gaatttctaa gtatgagtta agtagtttca 180
 ttgctgactt taagcatttc aaaccagggg acaccgtacc agaaatgtac cgtaccgatg 240
 agtacaacat taagcagtgg cagttgcgta acctgcccgc gcctgatgcc gggacgcaact 300
 ggacctatat ggggtggcgcg tacgtgttga tcagcgacac cgacggtaaa atcattaaag 360
 cctacgacgg tgagatTTTT tatcatcgct aaaaaagcc ccctcatcat gagggggaaa 420
 tgcagacacc ttgttatttt ttattattag ccacttgctc gtcttgcttg ttattagtcg 480
 tatttcacgt tgattaatgc ggttgccctcc agtgcgccag atttaacttt gtttgtatcg 540
 tagacgtagt aactggctgt atcgaa 566

<210> 440
 <211> 339
 <212> DNA
 <213> Escherichia coli

<400> 440
 cgtattcaca tccttttgat tgggtgataac atgcgaatcg gtattatttt tccggttgta 60
 atcttcatta cagcggctcg attttttagca tgggttttta ttggcggcta tgctgccccg 120
 ggagcataaa gatgaaaaaa acaacgatta ttatgatggg tgtggcgatt attgtcgtac 180
 tcggcactga gctgggatgg tggtaacgtc acctctaaaa aatagcaaag gctgcctgtg 240
 tgcagccttt gtgcaattta agcgttaact tttaatcttc ctgtagataa atagcacgac 300
 aatcgcacca ataacggcaa ccacgaagct gccaaaatt 339

<210> 441
 <211> 376
 <212> DNA
 <213> Escherichia coli

<400> 441
 catgaatatt taaaaaggaa aacgacatga aaccgaagca cagaatcaac attctccaat 60
 cataaaatat ttccgtggag cattttatta ttgaatatag aggtttaact ccggtaaaaa 120
 acaaagaagc attgaatgca gggaaaaata atatggccat aaaaaacatc gaaagaaact 180
 cttttaattt aacatgtaaa cgcattggtta atcctcatat cacgggtgga gtgttaagaa 240
 catacataaa tggagtcatt ttttcccttt tccatttatc aagttcctgt tgccgtttta 300
 gtccatctct aattgcatat ttttaatttt ctgataaatg gcattgagca tcgatttcat 360
 ttaaaacaac tgtaca 376

<210> 442
 <211> 446
 <212> DNA
 <213> Escherichia coli

<400> 442
 ttacgatagc tattagtaaa aatataagag ttagctgtat tgttatgtct gtggcgaaat 60
 tgactacctt cgtttttttg attaagaatg attttattat cgtaagtaaa attacatgaa 120
 tattttaaaa ggaaaacgac atgaaaccga agcacagaat caacattctc caatcataaa 180
 atatttccgt ggagcatttt attattgaat atagagggtt aactccggtg aaaaacaaag 240
 aagcattgaa tgcaggggaa aataatatgg ccataaaaaa catcgaaaga aactctttta 300
 atttaacatg taaacgcatg gttaatcctc atatcacggg tggagtgtta agaacataca 360
 taaatggagt catgttttcc cttttccatt tatcaagttc ctgttgccgt tttagtccat 420

ctctaattgc atattttaat ttttct

446

<210> 443

<211> 388

<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<222> (1)...(388)

<223> n = A,T,C or G

<400> 443

tcaccccggt	gccgattttc	aggcatcctg	atttaactta	gcacccgcaa	cttaactaca	60
ggaaaacaaa	gagataaatg	tctaatacctg	atgcaaatacg	agccgatttt	ttaatcttta	120
cggactttta	cccgcctggt	ttattaattg	caactgtnatc	cgggcgttcg	cccgccttta	180
tcacaatagg	ctgtgtagcc	tgggcctggt	tctctttcac	ccgcgccaga	gcggcagcaa	240
tgcacatctt	atctttggct	gcaggttgaa	cggctgcgct	cttatgtcgt	tcaaggcgag	300
ccgctttttc	gcgctccaga	cgagcctggc	gcgcttcgaa	acgcgctttg	gcttctgcgg	360
cncgcttttc	ttcctgacga	atagccgc				388

<210> 444

<211> 209

<212> DNA

<213> Escherichia coli

<400> 444

aattttaata	acgctatctg	cggataaagc	agaatagggtg	gttaacccca	gacataaacc	60
gaggaaaata	atgttattgt	atttcataat	ctattgttcc	ttagcgacag	attgctgtct	120
gctgggttcag	taaggtagca	ggagaaactt	caggaagctt	gtactcgaca	atacagtttg	180
agtttttata	tttgcccat	gaaacctgt				209

<210> 445

<211> 341

<212> DNA

<213> Escherichia coli

<400> 445

catcctcaat	accgttaaat	gcaacccgaa	cccccgttgt	ccctttgctg	cattcaactta	60
acgtaatactg	aaaagggagc	gctggacttg	tgctaccggt	cgttggaat	tgtctggcac	120
tgtttttttg	gagatctacg	gtaaaattaa	gcgaatccga	tgagactgtg	cagccataat	180
cgaggagcgc	cccgcctaatt	ttaataacgc	tatctgcgga	taaagcagaa	taggtgggta	240
acccagagaca	taaaccgagg	aaaataatgt	tattgtattt	cataatctat	tgttccttag	300
cgacagattg	ctgtctgctg	gttcagtaag	gtaccaggag	a		341

<210> 446

<211> 697

<212> DNA

<213> Escherichia coli

<400> 446

agattttactg	ccaattttccg	gcagatcgga	aagggttaam	ccatattgat	ccataagggt	60
acgaatcmcg	ggctataccg	ccaggcatgg	cttgagccat	ggcattaaat	tccgcaaatt	120
cgggcgctga	ttcttccac	gcggttattt	tggcacacac	cagatccagc	aagggtttt	180
caggatcggt	gagcagcaga	tgatctacca	gttccagcgc	ctgggtgtat	tgttcctcgt	240
tctgaatacc	cgccagaaaa	ggtgccacag	cagttagctt	ttctcctgct	tgcaagatgt	300
cggcaatcgc	aatcattttt	tccccttagt	acgatgaaca	gcggtaaaga	aatcgtattc	360

tttatgcgtc	ataacttcac	gtatgtagca	cttttgcat	tcaaaaaaga	ccattgctac	420
aacacgtaat	tcattgcccc	caacattgaa	aacataatgc	ttatccagat	atttgaagtt	480
atccagagat	gggaatactg	cttttaaatga	ctcaggtttt	ttgaaatata	ccttagcaat	540
cgtgktcccc	agagccacca	actccgtttt	atgttgcggg	tatttttccg	cagcatcttt	600
caatgctttt	tgagttatca	ggtgcattct	tcatacgtc	cgtkgmcaaa	ttggcaatat	660
gataacatcc	gttgccagat	tggcacggat	gaattat			697

<210> 447

<211> 215

<212> DNA

<213> Escherichia coli

<400> 447

aattaataac	ttttcgttag	gcagtttttg	gtgtgagttg	caagagggga	gactactgaa	60
taactcaagt	tttataatcg	aggggaaaat	ggtgatggcg	ttcatagcaa	aacgccctca	120
accataaagg	tcgagggcgc	ttaagatgtt	aaaaacccgc	tatccgttaa	aaaacaatgt	180
tcaactaagg	tcagtgcacat	tgcgctaata	aagcg			215

<210> 448

<211> 395

<212> DNA

<213> Escherichia coli

<400> 448

gcattattca	tgagaaatgt	gtatcgtaaa	tcaactgaaa	ttaacgcaac	catttgttat	60
ttaaggttta	attatctgtg	tgtgatattt	tattgaatgt	tttaaataat	gtttttattg	120
gcattgctat	aattattggt	atcatttgct	gaatggattc	agtcttaatg	agtgggtttt	180
taagggacag	gcataagata	atgatacgta	tgcataacca	acatctttac	tcattatgtc	240
attgaatggt	gacgctatgt	gtttatgagg	gagaggtatt	ttcagttgat	ctggattgtt	300
aaattcatat	aatgcgcctt	tgtcatgaa	tggatgccag	tatgtagtgg	gaaattataa	360
atattgaaat	agtccaacta	cttctttatt	accaa			395

<210> 449

<211> 641

<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<222> (1)...(641)

<223> n = A,T,C or G

<400> 449

ataatcaggt	aagaaaagg	gcgcggagat	taccgtgtgt	tgcgatatat	tttttagttt	60
cgctggcaa	tacatcagtg	gcaataaaac	gacatatcca	gaaaaatata	cactaagtga	120
atgatattct	cagatttatc	ttaatcgttt	atggataacg	gcaaagggtc	tcgttttttc	180
ctatacttat	tcagcactca	caaataaagg	aacgccaatg	aaaattatac	tctgggctgt	240
attgattatt	ttcctgattg	ggctactggg	ggtgactggc	gtatttaaga	tgatatttta	300
aaattaatta	atgtcatcag	gtccgaaaa	aacgagaata	tttcagttct	tcatacctgt	360
gcgctcctgt	catgtgcatt	gcttcatata	atcactggcg	caaggagcgc	cgcaggcgna	420
gnntgcncgn	cgncaccct	naccccatgc	cgaacttcag	aantgaaaac	nccntaacnc	480
cgatngtcgg	cggngcctc	cccatgcnan	agtangggaa	ntgccangcg	ncnnattaaa	540
cgaaggctn	attncaaaga	ctgggccttn	cntttatctg	atgtttgtcg	gagaacgctc	600
tcctgagnan	gacaaatncc	gcggggagcg	gatttgaacn	t		641

<210> 450

<211> 314

<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)..(314)
<223> n = A,T,C or G

<400> 450
gaactacgag taagaatagc tncgaattcc cgtttatgga taacggcaaa gggcttcggt 60
ttttcctata cttattcagc actcacaaat aaaggaacgc caatgaaaat tatactctgg 120
gctgtattga ttattttcct gattgggcta ctgggtggtga ctggcgtatt taagatgata 180
ttttaaaatt aattaatgtc atcagggtccg aaaataacga gaatatttca gtctctcatc 240
ctggtgcgct cctgtcatgt gcattgcttc atataatcac tggcgcaagg agcgcgcagg 300
gggntntnnt cttt 314

<210> 451
<211> 236
<212> DNA
<213> Escherichia coli

<400> 451
atatacacta agtgaatgat atcttccgat ttatcttaat cgtttatgga taacggcaaa 60
gggcttcggt ttttcctata cttattcagc actcacaaat aaaggaacgc caatgaaaat 120
tatactctgg gctgtattga ttattttcct gattgggcta ctgggtggtga ctggcgtatt 180
taagatgata ttttaaaatt aattaatgtc atcagggtccg aaaataacga gaatat 236

<210> 452
<211> 418
<212> DNA
<213> Escherichia coli

<400> 452
cggagattac cgtgtgttgc gatatatattt ttagtttcgc gtggcaatac atcagtggca 60
ataaaacgac atatccagaa aaatatacac taagtgaatg atatcttccg atttatctta 120
atcgtttatg gataacggca aagggtctcg ttttttccta tacttattca gcactcacia 180
ataaaggaac gccaatgaaa attatactct gggctgtatt gattattttc ctgattgggc 240
tactggtggt gactggcgta ttttaagatga tattttaaaa ttaattaatg tcatcaggtc 300
cgaaaataac gagaatatatt cagtctctca tcctgttgcg ctccgtgcat gtgcattgct 360
tcatataatc actggcgcaa ggagcgcgca gggggcggcc aatcgccgcc gccccctg 418

<210> 453
<211> 551
<212> DNA
<213> Escherichia coli

<400> 453
aacaatttgc ccatgcgctc ggtcatgcgc tgcacgccc ggccattttg sgcgcccccg 60
cgaccgccat tgcactgtta atgggogaat cttcagtaact ggtattaggt ggacaacgcg 120
cgctgcctaa acggctggaa gaagcgggtt ttgcgtttcg ctggtacgat ttagaagagg 180
cgctggcgga tgtcgttcgc tgatgtggtt tacagcaaac atccgccagt taactccccg 240
tgttacagga ttagtggtct tgcgcgataa gatcgtctgg tgaaagtcgg gtcaccatca 300
taactaactc tctgtctaaa cctctatcca gcactctctg agcaatacgc agggcttctt 360
cgtgtttgcc ctgcattgog ccttcttcac gtaatctgtc agcaatggtc atcaagtttc 420
tccttttctt gtgggtgcgcg ttccgctatc tcaccaataa atgcacgaaa acgctgggca 480
tccctgtttt gtaatacgtg attaaacagg gcttttagct gtctgtcatt agtgktccct 540
gtaactagca g 551

<210> 454
 <211> 93
 <212> DNA
 <213> Escherichia coli

<400> 454
 tggcatctcg gtgtttgccga tcttcatgat atccagcccg ccggaactt cttcccaaac 60
 ggttttgctg ttatccattg agtcacggaa ctg 93

<210> 455
 <211> 232
 <212> DNA
 <213> Escherichia coli

<400> 455
 cgtgccgaga tgatcctgta accatcatca gttgtgaagt agtgattcac gacttcaagg 60
 cgcttttcaa aaggggtattt tggctttgac atattagggg ctattccatt tcatcgcca 120
 acaaaatggg tgcagtacat actcgttggg aatcaacaca ggaggctggg aatgccgcag 180
 aaatatagat tactttcttt aatagtgatt tgtttcacgc ttttattttt ca 232

<210> 456
 <211> 713
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(713)
 <223> n = A,T,C or G

<400> 456
 ttagnggatn naangccac ancctcgang gatctaggag gtagaatagc ttcgaattcc 60
 ccagcagagc gcggccttct tcgtcagatt tcgcagtagt ggtaatggta atatccaaac 120
 cacgaacgcg gtcgacttta tcgtagtcga tttctgggaa gatgatctgc tcacggacac 180
 coatgctgta gttaccacga ccgtcgaaag acttagcgga caggccacgg aagtcacgga 240
 tacgaggtag agcaatagtg atcaggcgct caaagaactc ccacatgctg tcgccacgca 300
 gagttacttt acagccgacg ggatagccct gacggatttt gaagcctgca acagatttgc 360
 gtgcttttgt gatcagcggg ttttgaccgg agattgctgc cagggtctgct gctgcgttat 420
 ccagcagttt tttgtcagcg atcgcttcac caacacccat gttcagggtg atcttctcga 480
 cccgagggac ttgcatgaca gaattgtagt taaactcagt catgagtttt ttaactactt 540
 cgtctttgta gtaatcatgc agtttcgcca tcgtactact ccagtgcggg gaacgctctc 600
 ctgagtagga caaatccgcc ggagccggat ttaacgttgc gaacaaccgn cccggagggg 660
 tggnggcagg accccgccat aactggcagc attaaattaa gcagaaggcc atc 713

<210> 457
 <211> 292
 <212> DNA
 <213> Escherichia coli

<400> 457
 tgaacagcag agatacggcc agtgcggcca atgttttttg tcctttaaac ataacagagt 60
 cctttaagga tatagaatag gggatatagc acgccagaat atcgattttg attattgcta 120
 gtttttagtt ttgcttaaaa atattgttag ttttattaaa tgcaaaacta aattattggg 180
 atcatgaatt tggtgtatga tgaataaaat ataggggggt atagatagac gtcattttca 240
 tagggttata aatgcgacta ccatgaagtt ttttaattgaa agtattgggt tg 292

<210> 458
 <211> 282
 <212> DNA
 <213> Escherichia coli

<400> 458
 ttattaaatg caaaactaaa ttattggtat catgaatttg ttgtatgatg aataaaatat 60
 aggggggtat agatagacgt cattttcata gggttataaa tgcgactacc atgaagtttt 120
 taattgaaag tattgggttg ctgataattt gagctgttct attcttttta aatatctata 180
 taggtctgtt aatggatttt atttttacaa ttttttgtgt ttaggcataat aaaaatcaac 240
 ccgccatatg aacggcgggt taaaatattt acaacttagc aa 282

<210> 459
 <211> 300
 <212> DNA
 <213> Escherichia coli

<400> 459
 tctgcgttcc gctaaaaggt gcaaattgctc aggacgttgc agcgttttgc gtgaccgctc 60
 ggggaaggca aaattgcctc tgggaaagca ttgcgcgggg tccggcgctc atcaacaatc 120
 ggggggcagc aaggggctga aacgggaaag cccctcccgga agaagggggc ttgtataagg 180
 aaaggggttat gatgaagctc gtcatacatc tggttgtgtt gttactgtta agtttcccgga 240
 cttactaaca actcatcaga gggggggagaa atcctccctt acccttggtc ctttactcta 300

<210> 460
 <211> 293
 <212> DNA
 <213> Escherichia coli

<400> 460
 cgggggtccg cgctcatcaa caatcggggg gcagcaaggg gctgaaacgg gaaagcccct 60
 cccgaagaag gggccttgta taaggaaagg gttatgatga agctcgtcat catactggtt 120
 gtgttggttac tgttaagttt cccgaacttac taacaactca tcagaggggg gagaaatcct 180
 cccttaccct tgttccttta ctctaggttg aaaaaacaac agcgtcaata ggctgccat 240
 gtacgaagcg agatctgtga accgctttcc ggtttagcctt ttttatcctg ttg 293

<210> 461
 <211> 359
 <212> DNA
 <213> Escherichia coli

<400> 461
 caacacagga ggctgggaat gcgcagaaa tatagattac tttctttaat agtgatttgt 60
 ttcacgcttt tattttttcac ctggatgata agagattcac tgtgtgaatt gcatattaaa 120
 caggagagtt atgagctggc ggcgttttta gcctgcaaat tgaaagagta agagtcttcg 180
 gcgggaaatt attccgcct tacttacggc gttgcgcatt ctattgcac ccaaatttat 240
 tcttcacaaa aataataata gattttatta cgogatcgat tatttatttc ctgaaaacaa 300
 ataaaaaat ccccgccaaa tggcagggat cttagattct gtgcttttaa gcagagatt 359

<210> 462
 <211> 673
 <212> DNA
 <213> Escherichia coli

<400> 462
 gcaacccatg tctgacctg ggttcggggg acacccaaac gtgccgagat gatcctgtaa 60
 ccatcatcag ttgtgaagta gtgattcacg acttcaaggc gcttttcaaa aggggtatttt 120

ggctttgaca	tattaggggc	tattccattt	catcgcccaa	caaaatgggt	gcagtacata	180
ctcgttggaa	atcaacacag	gaggctggga	atgccgcaga	aatatagatt	actttcttta	240
atagtgattt	gtttcacgct	tttatttttc	acctggatga	taagagattc	actgtgtgaa	300
ttgcatatta	aacaggagag	ttatgagctg	gcggcgtttt	tagcctgcaa	attgaaagag	360
taagagtctt	cggcgggaaa	ttattcccg	cttacttacg	gcgttgcgca	ttctcattgc	420
acccaaattt	attcttcaca	aaaataataa	tagattttat	tacgcgatcg	attattttatt	480
tcctgaaaac	aaataaaaaa	atccccgcca	aatggcaggg	atccttagatt	ctgtgctttt	540
aagcagagaa	tacaggctgg	ttacgttacc	agctgccggg	cctttagcgc	cgctttcgat	600
ggtgaaggac	actttctgac	cttcgtccag	agatttgtaa	ccatcgttct	ggatagcaga	660
gaagtgtacg	aac					673

<210> 463

<211> 630

<212> DNA

<213> Escherichia coli

<400> 463

tggtggcatt	ggttgctgga	gagagaaaac	ccccgcacgt	tgcaggtatg	cacctgacaa	60
caccacgggg	gctaattctt	actctagacc	actcaagaat	agccgcgaaa	cgttgtcatt	120
acaacacagg	cggctatatg	acgttcgcag	agctgggcat	ggccttcttg	catgatttag	180
cggctccggg	cattgctggc	attcttgcca	gtatgatcgt	gaactggctg	aacaagcgga	240
agtaacgtgt	catgcggggc	tcaggctgcc	gtaatggcaa	tttgcgccc	gaccaggccg	300
caggggggaa	actctgcggc	ctttttcgtt	cttactgcgg	gtaaggcacc	cagtcgccgc	360
cgttcaggcg	aacgtacggg	ttatcctggg	attgaataac	tactgcattt	gagttctcgg	420
agaccggtgc	tgttttgtgg	aacccaactg	tgagtttttt	ccagtcaaca	ttgtcttcgg	480
tgaaaatctt	gccatcgaga	acgcgaacca	ccagatcgga	gatagccagg	aagctgctcg	540
gttgttcgat	gacaatcggt	gccccctgat	gcgggtgcct	catgccgaag	aatttcaccc	600
caacggggac	gtcggtgata	gacgggctag				630

<210> 464

<211> 391

<212> DNA

<213> Escherichia coli

<400> 464

ctcaggctgc	tgattgtttt	tttgtgcaat	ggcgcggtat	tagcgtcgtt	gctgtcgatg	60
gagagaatca	taaacgtggg	gaatgatgat	tgtagcaag	gaaaactgtc	aaaaatcttc	120
aaaaaatttg	agggataagg	ccggaatggc	tcgggccaga	gggaagttaa	ccgcgaagct	180
gttgetgctt	gagggctcgt	ttaaccagac	gccaggcgct	ccatacgcca	aaaccgcgtc	240
tggcccagcg	gaccagcata	ttaggatggc	gaatcgtcca	gatcgccatc	acgctactgc	300
caaccagcgc	ccaggagcgc	agacttagca	gcatattcca	gcgacgatcg	taagcgctcg	360
ttgtctccag	ccattcacga	cgactggcgg	a			391

<210> 465

<211> 625

<212> DNA

<213> Escherichia coli

<400> 465

aacacaccac	accataaacg	gaggcaaata	atgctgggta	atatgaatgt	tttaatggcc	60
gtactgggaa	taattttatt	ttctggtttt	ctggccgcgt	atttcagcca	caaatgggat	120
gactaatgaa	cggagataat	ccctcaccta	accggcccct	tgttacagtt	gtgtacaagg	180
ggcctgattt	ttatgacggc	gaaaaaaaac	cgccagtaaa	ccggcggtga	atgcttgcac	240
ggatagattt	gtgtttttgt	tttacgctaa	caggcatttt	cctgcactga	taacgaatcg	300
ttgacacagt	agcatcagtt	ttctcaatga	atgtaaaacg	gagcttaaac	tcggttaatc	360
acatttttgt	cgtcaataaa	catgcagcga	tttcttcggg	tttgcttacc	ctcatacatt	420
gcccgggtccg	ctcttccaat	gaccacatcc	agaggctctt	caggaaatgc	gcgactcaca	480

cctgctgtca	cggtaatgtt	gatatgccct	tcagaatgtg	tgatggcatg	gttatcgact	540
aactggcaaa	ttctgacacc	tgacgacat	gcttcttcat	cattagccgc	tttgacaata	600
atgataaatt	cttcgcccc	gtagc				625

<210> 466
 <211> 623
 <212> DNA
 <213> Escherichia coli

<400> 466	
tgcttttgaa	60
taatgtgtcg	
caatcttgag	
aaggaaatgg	
cgaccacgaa	
agaaaaggca	120
aaaacgataa	
tctgaaagag	
ccaaggtatt	
tcagtataag	
cattgaatgc	
gacagtaaac	180
tctttcggta	
tcagccagag	
agttagacca	
aaaatgataa	
tcgtatacat	
aagtctttcg	240
agtggctcgt	
tagcaaaaag	
tttcaacaat	
ggagtaaata	
catccaacat	
atcaataact	300
ctcaactgta	
aggggtattga	
aatgttaaca	
caagctctcg	
ctgtaggggt	
atagccgaga	360
ccaccgaagc	
ccggaggtgg	
tgaaataaaa	
ccgggcacaa	
cacgaaggcg	
catttccgat	420
atccataaag	
agtcgggtctt	
gtctgtttaa	
tttaaattgg	
gggagtgcgc	
ctccggttgt	480
aaataacgac	
attgctgtgt	
gtagtcctgg	
cggcacatcag	
ttttttcttg	
aagttcggct	540
gatgtccgcc	
cttttttaag	
tgaattttgt	
gatgcggtga	
atgcggctaa	
gcgcacgtgg	600
cacagttaaa	
agtcattgta	
gtccttattg	
gtttgggtgg	
gaaagccgac	
tgtaattgtt	623
aactggttgc	
agtcacctgg	
agg	

<210> 467
 <211> 234
 <212> DNA
 <213> Escherichia coli

<400> 467	
tgtttactta	60
caagagattc	
atctttgtat	
aaataaagat	
aagtaattac	
gcataaaaaca	120
acaatgatta	
taatagcaaa	
aataaatatt	
atcatctttg	
atagattact	
tgagatagcc	180
agcatcttgt	
aaagccttta	
tcgttttttt	
atgctctgga	
ttaatataat	
cactacatct	234
atctgagcaa	
tctgttgttg	
atggacatgt	
caaccatgg	
tcattttacag	
ccaa	

<210> 468
 <211> 529
 <212> DNA
 <213> Escherichia coli

<400> 468	
attagctatt	60
tcggctaaaa	
tagagactac	
atgtcttcgg	
tccatctcac	
ttaaggagtg	120
tagttccggt	
gtaagttttt	
ccatagcttg	
cactgctaaa	
tttcgaacaa	
ggaattttct	180
gctggtaatc	
tctaaaaaga	
tggtcatggt	
tacaatgatt	
tttgtttctt	
tttgattatt	240
atgaacaact	
gtccatgatt	
tcgttttaaga	
atgaagagaa	
atcactaaac	
gaactgaata	300
tattttctgt	
gccaatatta	
tctctaattt	
caaaaaagtt	
acttttaattg	
tcggtaatga	360
ctccaactta	
ttgatagtgt	
tttatgttca	
gataatgcc	
gatgactttg	
tcatgcagct	420
ccaccgattt	
tgagaacgac	
agcgacttcc	
gtcccagcgc	
tgccaggtgc	
tgccctcagat	480
tcaggttatg	
ccgctcaatt	
cgtgcgtat	
atcgcttttc	
cttatcagtt	
cgttgatgtc	529
agtggttttg	
accacgaggg	
agcttcacgc	
gagttattga	
aaaccctga	

<210> 469
 <211> 261
 <212> DNA
 <213> Escherichia coli

<400> 469	
caaagaacct	60
tcaacatgaa	
aaatatccat	
ttgtttgcaa	
aaaaagatta	
ttaggaagga	120
aattaatgca	
attatcgaaa	
attcaaaaaa	
tatccaaaaa	
tagtataact	
tattccagaa	

gagttcaata taatgtttgt cttcaatfff tcttacttca gggtaatata gattgctcat	180
tacattgtga gcttcatctt tatttaatff tctgttgact ccagctctcc gtgataacgg	240
ttttataatt agatgcttat c	261

<210> 470
 <211> 98
 <212> DNA
 <213> Escherichia coli

<400> 470	
agatgattgc cgggaacttg ttagcggcac gcaggcggcg gctcgcaccc ttaccctgct	60
ctttacgtac ttctgcgttg atagtaaaca tttctttc	98

<210> 471
 <211> 259
 <212> DNA
 <213> Escherichia coli

<400> 471	
agcgcgaacg aagtcgatgt gctgcagctt cggtttgtac gggtgacgct gtacgtcctg	60
agcttttaact ttgatttctt taccgtaaac aacgatggtc agaacttcgc tgtagaattc	120
agcttttagct tgcattgttca tgactttgtc gtgatccagc tcgatagcca gcggcgcttc	180
tttgccaccg tagatgattg cogggaactt gttagcggca cgcaggcggc ggctcgcacc	240
cttaccctgc tctttacgt	259

<210> 472
 <211> 94
 <212> DNA
 <213> Escherichia coli

<400> 472	
aaaaacggcg taaagaaagg atgcaaacat gttaataaaa actcaaattg atcccacgta	60
tatattacgc cgcaaaaatcc ttacaataaa cagg	94

<210> 473
 <211> 174
 <212> DNA
 <213> Escherichia coli

<400> 473	
ttaattatta aaatagtgt aacgcgattat gtggttatgg gggtaaacad taaataaacc	60
agcggggagg ggaggtaaag tgaaaaaata aaaagcggat aatcttaata agcaggccgg	120
acagcatcgc catccggcac tgatacaggg tttatttcag ctcatcaacc atcg	174

<210> 474
 <211> 138
 <212> DNA
 <213> Escherichia coli

<400> 474	
ctgtaaaaac gtcaaaaaga gtgttttatc aacagaagaa tggaggctctg acagatagta	60
gtaatgcaaa aaaatggaga cttaagttga atgaacggga gtaaagcgaa aagactatag	120
agtgaaggag aaattccc	138

<210> 475
 <211> 191
 <212> DNA

<213> Escherichia coli

<400> 475

tttggttggt	taatatctta	ttgttatctt	tatttataga	tgtttatatt	gcatgaggtg	60
gtttttggag	agaagaatga	ggaagatgcg	tcgagccaca	gaaacgttag	ctttacatat	120
agcggaggtg	atgtgaaatt	aatttacaat	agaaataatt	tacatatcaa	acagttagat	180
gctttttgtc	g					191

<210> 476

<211> 245

<212> DNA

<213> Escherichia coli

<400> 476

cggccattta	tacaggaaaa	gcctatgtca	gaacgtaaaa	actcaaaatc	acgccgtaat	60
tatctcggtt	aatgtttcctg	cccaaactgc	acccaagagt	cagaacacag	tttttcaaga	120
gtacaaaaag	gtgccctttt	gatctgccct	cattgcaaca	aagtattcca	gacaaatctt	180
aaagctgtag	cctgattgat	tttattagta	acaagtattt	tttatatttt	aataatatat	240
ttaaa						245

<210> 477

<211> 319

<212> DNA

<213> Escherichia coli

<400> 477

aaattttcag	gtaccttgct	accatacttt	tttttctgag	cattaatgat	attttgagct	60
tcttgaggat	ctttaactcc	ccacatttgg	tggaaagtat	tcatattaaa	aggaagggtg	120
aataatttgt	ctttataaat	cgccagtgga	gaattagtaa	aacgattaaa	ttctactaaa	180
tcattaacgt	aatcccatat	atatttatca	ttggtagtaa	aaatatgtgc	accatattta	240
tgaatctgga	taccctcaca	gtcctctgtg	tacgcatttc	caccgatatg	atttcttttc	300
tcaatcacta	aaacttttt					319

<210> 478

<211> 149

<212> DNA

<213> Escherichia coli

<400> 478

gcagtgatcg	aagcgatgac	gaagtgtatg	gaaaaatcag	aaaaactcag	caaatcctga	60
tgactttcgc	cggacgtcag	gcgcgccactt	cggtgcgggtt	acgtccgggt	ttctttgctt	120
tgtaaagcgc	caaatctgcc	gatttcaac				149

<210> 479

<211> 330

<212> DNA

<213> Escherichia coli

<400> 479

gaaagtatct	tcgttattga	catcactgga	aaatataact	tgcttttcat	tattaaactc	60
gaagcgcgta	ccgtatctgg	acaaacattt	atcgagctta	ccaaattcct	gaagagggtt	120
aactacagat	aacatttgcg	cgtcctttgc	agtaatgcc	gtcaaactcct	tgacgggcat	180
tatttagatt	aaattaccag	tatttcttcg	gagtgaagaa	tattaccagg	tatatttaac	240
accacggttc	gcggaccagt	cttgatctac	gtcaccacca	ccgaggtagt	tagcatcggt	300
ataggcgctg	aagttcttgg	tgaagctaaa				330

<210> 480

<211> 191
 <212> DNA
 <213> Escherichia coli

<400> 480
 tttttttcca gcaacggagc aaaagggttg cccttggtgca gctcagggtt aaccacttta 60
 actacgtggc gacgacccgg agatgtcggg ttacatttaa caactgccat tgtattactc 120
 ctccgactta ctcagcgccg ccaacgaagt ccagattctg gccttctttc agggtgacgt 180
 aagctttttt c 191

<210> 481
 <211> 188
 <212> DNA
 <213> Escherichia coli

<400> 481
 tccctttaac taccagggtg ttaacgactt cgacttcgac ttcaaacagt ttctgcacag 60
 cagctttgat ttctgctttg gtcgcgtctt tagcaacttt gactacgatg gtgttggtt 120
 tttccatcgc agtagacgt ttttcagaaa cgtgcggtgc acgcagcacc ttcagcagac 180
 gttcttca 188

<210> 482
 <211> 172
 <212> DNA
 <213> Escherichia coli

<400> 482
 caaaggcgaa caaagcctgt gaagcccgaa ggctccacag acagtgtctac ttgaaggcct 60
 tactgtttct tcttaggagc gaggaccatg atcatctggc ggccttcgat cttcggtggg 120
 aaggattcga ccaactgccg ttcttgcaaa tcgtctttca cgcgattaag ca 172

<210> 483
 <211> 266
 <212> DNA
 <213> Escherichia coli

<400> 483
 tggagaaaac ggggtgattga taaagcaatc atcgttctag gggcggttaat tgcgctgctg 60
 gaactgatcc gctttctgct tcagcttctg aactgatagc ggaaacgtaa ttaagggcta 120
 agagcacact actcttagcc ctttaacatt taacgcattg tcacgaactc ttctgcgcgc 180
 gttgggtgaa tggcgacggg attgtcgaag tcttttttgg ttgcccccat cttcagcgcc 240
 accggaagc cctgcaacat ttcgtc 266

<210> 484
 <211> 259
 <212> DNA
 <213> Escherichia coli

<400> 484
 cgcaggcagc tgatggtcaa caggatgaga gaaaccgaga gacagggtta tcaattgcc 60
 ttttaaccgt gcacggtaac ctacaccaac cagctgcagc ttcttagtga agccttcggg 120
 aacaccgata accattgagt tcagcagggc acgcgcggtg ccagcctgtg cccaaccgtc 180
 tgcgtaacca tcacgcggac cgaaggtcag ggtattatct gcatgtttta cttcaacagc 240
 atcgttgaga gtacgagtc 259

<210> 485
 <211> 73

<213> Escherichia coli

caggtcggaa cttacccgac aaggaatttc gctacottag gaccggtata gttacggccg
ccgtttaccg ggg

73